STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 105257

TO: Phillip Gambel
Location: CM-1/9E12
Art Unit: 1644
Wednesday, October 08, 2003

Case Serial Number: 09/155739

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Gambel,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

sira
Search and Information
Resources Administration

OM protein - protein search, using sw model

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              GenCore version 5.1.6
           Copyright (c) 1993 - 2003  Compugen Ltd.
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Run on: October 7, 2003, 09:01:50 ; Search time 53.6727 Seconds
                   (without alignments)
                   363.748 Million cell updates/sec

Title: US-09-155-739-11
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKV.........NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                   Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	655	100.0	123	16	AAR81323	Humanized VLA-4 an
2	655	100.0	142	16	AAR81333	Human VLA-4 reshap
3	655	100.0	142	18	AAW22428	Humanised alpha-4
4	648	98.9	123	18	AAW22413	Humanised alpha-4
5	552	84.3	123	16	AAR81330	Mouse anti-VLA-4 a
6	544	83.1	140	16	AAR81327	Mouse VLA-4 antibo
7	544	83.1	140	18	AAW22410	Alpha-4 integrin m
8	523.5	79.9	120	19	AAW44124	Heavy chain variab
9	523.5	79.9	120	23	AAU79034	Humanised antibody
10	523.5	79.9	431	22	AAB30693	A fusion of single
11	523	79.8	136	16	AAR76681	Human/murine chime
12	523	79.8	136	17	AAW04396	Chimaeric human/mu
13	523	79.8	269	16	AAR76682	Human ONS-M21 anti
14	523	79.8	269	17	AAW04397	Chimaeric human/mu
15	515	78.6	119	16	AAR81325	Humanized VLA-4 an
16	515	78.6	119	18	AAW22426	Humanised alpha-4
17	512	78.2	119	16	AAR81324	Humanized VLA-4 an
18	512	78.2	119	18	AAW22425	Humanised alpha-4
19	507.5	77.5	135	21	AAB07969	A heavy chain vari
20	505.5	77.2	258	23	ABB05963	Monoclonal antibod
21	505.5	77.2	258	23	ABB05992	Mouse and human ch
22	505.5	77.2	258	23	ABB05996	Human monoclonal a
23	504.5	77.0	118	14	AAR37611	hIL2R Ab H chain V
24	503	76.8	119	20	AAY52717	Humanised ATR-5 H
25	503	76.8	119	22	AAB74978	Humanised ATR-5 H
26	501.5	76.6	258	23	ABB05991	Mouse and human ch
27	501.5	76.6	258	23	ABB05995	Human monoclonal a
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29	499	76.2	119	22	AAB74980	Humanised ATR-5 H
30	496	75.7	136	17	AAR92084	Humanised antibody
31	496	75.7	136	23	ABG31443	Amino acid sequenc
32	495	75.6	119	16	AAR81331	Human 2*CL antibod
33	493	75.3	119	20	AAY52718	Humanised ATR-5 H
34	493	75.3	119	22	AAB74979	Humanised ATR-5 H
35	492	75.1	117	15	AAR57476	CDR-grafted anti-R
36	492	75.1	117	17	AAR92079	Murine 1308F VH CD
37	492	75.1	117	23	ABG31426	Humanised CDR-graf
38	492	75.1	136	15	AAR57481	Humanized 1308F VH
39	491.5	75.0	245	23	ABP45885	Human BLyS binding
40	491	75.0	119	20	AAY52708	Humanised ATR-5 H
41	491	75.0	119	22	AAB74969	Humanised ATR-5 H
42	489.5	74.7	120	18	AAW27551	Human Ab heavy cha
43	489	74.7	119	20	AAY52720	Humanised ATR-5 H
44	489	74.7	119	22	AAB74981	Humanised ATR-5 H
45	487.5	74.4	120	15	AAR47491	Humanised anti-CD1

ALIGNMENTS

RESULT 1
AAR81323
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ID   AAR81323 standard; Protein;  123 AA.
XX
AC   AAR81323;
XX
DT   02-APR-1996  (first entry)
XX
DE   Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;  95WO-US01219.
XX
PR   25-JAN-1994;  94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
```

Claim 11; Page 69; English.

The sequence encodes the mouse antibody 21.6 heavy chain variable region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and for treating inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.

SQ Sequence 123 AA;

Query Match 100.0%; Score 655; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 7.2e-53;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Qy 121 VSS 123
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Db 121 VSS 123
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RESULT 2
AAR81333
ID AAR81333 standard; Protein; 142 AA.
XX
AC AAR81333;
XX
DT 23-MAR-1996 (first entry)
XX
DE Human VLA-4 reshaped antibody 21.6 light heavy variable region.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "signal peptide"
FT Region 20..49
FT /note= "framework region 1"
FT Region 50..54
FT /note= "complementarity determining region 1"
FT Region 55..68
FT /note= "framework region 2"
FT Region 69..85
FT /note= "complementarity determining region 2"
FT Region 86..117
FT /note= "framework region 3"
FT Region 118..131
FT /note= "complementarity determining region 3"
FT Region 132..142
FT /note= "framework region 4"

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PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
DR N-PSDB; AAQ99894.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX
PS Disclosure; Fig 11; 105pp; English.
XX
CC The sequence represents the human reshaped antibody 21.6 heavy
CC chain variable region against leukocyte adhesion molecule VLA-4.
CC Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ99889)
CC regions are linked to human constant regions in the construction
CC of a humanized antibody against VLA-4. The 5' and 3' ends of the
CC mouse cDNAs are modified using PCR primers (AAQ99895-98) and then
CC subcloned into mammalian cell expression vectors containing human
CC kappa or gamma-1 constant regions. In the humanized heavy chain,
CC amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR
CC framework are replaced by the amino acid present in the equivalent
CC position of the mouse 21.6 Ig H chain. Plasmids encoding the
CC chimeric antibodies are transfected into COS cells. The humanized
CC antibodies can be used to inhibit adhesion of a leukocyte to an
CC endothelial cell and to treat inflammatory diseases such as multiple
CC sclerosis. They can also be used in the treatment of stroke,
CC cerebral traumas, meningitis or encephalitis. The antibodies can
CC also be used for detecting VLA-4, for affinity purification or for
CC generating anti-idiotype antibodies.
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SQ Sequence 142 AA;

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Best Local Similarity 100.0%; Pred. No. 8.4e-53;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 VSS 123
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Db 140 VSS 142
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RESULT 3
AAW22428
ID AAW22428 standard; Protein; 142 AA.
XX
AC AAW22428;
XX
DT 09-DEC-1997 (first entry)
XX
DE Humanised alpha-4 integrin antibody 21.6 VL version Ha.
XX
KW Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW metastasis; inflammatory bowel disease; rheumatoid arthritis;

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           GenCore version 5.1.6
           Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  7, 2003, 09:10:55 ; Search time 15.903 Seconds
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Title:          US-09-155-739-11
Perfect score:  655
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Scoring table:  BLOSUM62
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Searched:       328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:     328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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2	655	100.0	123	5	PCT-US95-01219-11	Sequence 11, Appl
3	655	100.0	142	2	US-08-561-521-17	Sequence 17, Appl
4	655	100.0	142	5	PCT-US95-01219-17	Sequence 17, Appl
5	552	84.3	123	2	US-08-561-521-9	Sequence 9, Appli
6	552	84.3	123	5	PCT-US95-01219-9	Sequence 9, Appli
7	544	83.1	140	2	US-08-561-521-4	Sequence 4, Appli
8	544	83.1	140	5	PCT-US95-01219-4	Sequence 4, Appli
9	523.5	79.9	120	4	US-08-871-488A-19	Sequence 19, Appl
10	523	79.8	117	3	US-08-646-265A-132	Sequence 132, App
11	523	79.8	136	3	US-08-646-265A-99	Sequence 99, Appl
12	523	79.8	269	3	US-08-646-265A-109	Sequence 109, App
13	515	78.6	119	2	US-08-561-521-13	Sequence 13, Appl
14	515	78.6	119	5	PCT-US95-01219-13	Sequence 13, Appl
15	512	78.2	119	2	US-08-561-521-12	Sequence 12, Appl
16	512	78.2	119	5	PCT-US95-01219-12	Sequence 12, Appl
17	505	77.1	125	2	US-08-561-521-44	Sequence 44, Appl
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19	495	75.6	119	2	US-08-561-521-10	Sequence 10, Appl
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21	492	75.1	117	5	US-08-290-592E-17	Sequence 17, Appl
22	492	75.1	117	5	PCT-US95-10053-14	Sequence 14, Appl
23	492	75.1	117	5	PCT-US96-09448-17	Sequence 17, Appl
24	492	75.1	119	4	US-09-438-954-41	Sequence 41, Appl
25	491.5	75.0	118	2	US-08-232-081B-8	Sequence 8, Appli
26	489.5	74.7	120	4	US-09-025-769B-36	Sequence 36, Appl
27	489.5	74.7	120	4	US-09-025-769B-59	Sequence 59, Appl
28	486	74.2	140	3	US-08-836-561-63	Sequence 63, Appl
29	486	74.2	140	1	US-09-434-122-63	Sequence 63, Appl
30	484.5	74.0	135	1	US-08-137-117D-112	Sequence 112, App
31	484.5	74.0	135	2	US-08-436-717-112	Sequence 112, App
32	484.5	74.0	139	1	US-08-253-877C-19	Sequence 19, Appl
33	484.5	74.0	139	2	US-08-452-164A-19	Sequence 19, Appl
34	484.5	74.0	139	3	US-08-603-02A-18	Sequence 18, Appl
35	484.5	74.0	139	1	US-08-450-809-14	Sequence 14, Appl
36	481	73.4	121	1	US-08-202-047-23	Sequence 23, Appl
37	481	73.4	121	3	US-08-964-690-23	Sequence 23, Appl
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43	473	72.2	123	1	US-08-482-882-53	Sequence 53, Appl
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45	473	72.2	123	2	US-08-487-113D-53	Sequence 53, Appl

ALIGNMENTS

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US-08-561-521-11
; Sequence 11, Application US/0856l521
; Patent No. 5840299
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend Khourie and Crew
;     STREET: One Market Plaza, Steuart Tower, Suite 2000
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94105
;   COMPUTER READABLE FORM:
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;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/561,521
;     FILING DATE:
;     CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/186,269A
;     FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Smith, William L.
;     REGISTRATION NUMBER: 30,223
;     REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-543-9600
;     TELEFAX: 415-543-5043
;   INFORMATION FOR SEQ ID NO: 11:
;     SEQUENCE CHARACTERISTICS:
;      LENGTH: 123 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-561-521-11

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Best Local Similarity   100.0%;  Pred. No. 2.7e-58;
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Qy 121 VSS 123
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Db 121 VSS 123

RESULT 2
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; Sequence 11, Application PC/TUS9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 123 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US95-01219-11

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Best Local Similarity 100.0%; Pred. No.2.7e-58;
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Qy 121 VSS 123

Db   121 VSS 123

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US-08-561-521-17
; Sequence 17, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC Compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/561,521
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/186,269A
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 142 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-17

Query Match   100.0%; Score 655; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.2e-58;
Matches 123; Conservative   0; Mismatches   0; Indels 0; Gaps 0;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 79

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 139

Qy 121 VSS 123
         |||
Db 140 VSS 142

RESULT 4
PCT-US95-01219-17
; Sequence 17, Application PC/TUS9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.

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               GenCore version 5.1.6

            Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:       October 7, 2003, 09:18:36 ; Search time 31.0606 Seconds
                                           (without alignments)
                                           626.523 Million cell updates/sec

Title:             US-09-155-739-11
Perfect score:     655
Sequence:          1 QVQLVQSGAEVKKPGASVKV.........NYGVYAMDYWGQGTLVTVSS 123

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters:       587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database   :     Published_Applications_AA:*
           1:  /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
           2:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
           3:  /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
           4:  /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
           5:  /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
           6:  /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
           7:  /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
           8:  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
           9:  /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
          10:  /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
          11:  /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
          12:  /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
          13:  /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
          14:  /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
          15:  /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
          16:  /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
          17:  /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
          18:  /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	523.5	79.9	120	15	US-10-056-794-19	Sequence 19, Appl
2	523.5	79.9	431	12	US-10-244-821-4	Sequence 4, Appli
3	523.5	79.9	431	15	US-10-013-173-4	Sequence 4, Appli
4	523.5	79.9	431	15	US-10-150-762-4	Sequence 4, Appli
5	523	79.8	117	11	US-09-749-873-132	Sequence 132, App
6	523	79.8	136	11	US-09-749-873-99	Sequence 99, Appl
7	523	79.8	269	11	US-09-749-873-109	Sequence 109, App
8	492	75.1	117	10	US-09-158-120A-17	Sequence 17, Appl
9	492	75.1	119	15	US-10-233-996-41	Sequence 41, Appl
10	491.5	75.0	245	11	US-09-880-748-1896	Sequence 1896, Ap
11	486	74.2	140	15	US-10-283-349-63	Sequence 63, Appl
12	485.5	74.1	120	14	US-10-025-687-2	Sequence 2, Appli
13	485.5	74.1	120	15	US-10-125-687-2	Sequence 2, Appli
14	484	73.9	180	9	US-09-748-960-6	Sequence 6, Appli
15	480.5	73.4	124	12	US-10-159-006-16	Sequence 16, Appl
16	480.5	73.4	124	12	US-10-159-006-41	Sequence 41, Appl
17	480.5	73.4	124	15	US-10-121-464-16	Sequence 16, Appl
18	479.5	73.2	252	11	US-09-880-748-1698	Sequence 1698, Ap
19	477	72.8	141	11	US-09-791-153A-60	Sequence 60, Appl
20	476.5	72.7	249	11	US-09-880-748-1290	Sequence 1290, Ap
21	476.5	72.7	249	11	US-09-880-748-1299	Sequence 1299, Ap
22	476.5	72.7	251	11	US-09-880-748-1146	Sequence 1146, Ap
23	475	72.5	119	15	US-10-233-996-4	Sequence 4, Appli
24	474.5	72.4	255	11	US-09-880-748-1156	Sequence 1156, Ap
25	474	72.4	140	15	US-10-283-349-74	Sequence 74, Appl
26	473	72.2	123	9	US-09-753-436-53	Sequence 53, Appl
27	473	72.2	123	15	US-10-269-805-27	Sequence 27, Appl
28	472.5	72.1	124	12	US-10-159-006-12	Sequence 12, Appl
29	472.5	72.1	124	12	US-10-159-006-40	Sequence 40, Appl
30	472.5	72.1	124	15	US-10-121-464-12	Sequence 12, Appl
31	472	72.1	123	9	US-09-753-436-86	Sequence 86, Appl
32	472	72.1	136	15	US-10-160-232-91	Sequence 91, Appl
33	470	71.8	136	11	US-09-749-873-29	Sequence 29, Appl
34	469.5	71.7	126	11	US-09-791-153A-61	Sequence 61, Appl
35	469.5	71.7	230	11	US-09-791-153A-53	Sequence 53, Appl
36	469	71.6	129	10	US-09-956-206A-77	Sequence 77, Appl
37	469	71.6	470	10	US-09-859-053-28	Sequence 28, Appl
38	468.5	71.5	124	12	US-10-159-006-14	Sequence 14, Appl
39	468.5	71.5	124	12	US-10-159-006-108	Sequence 108, App
40	468.5	71.5	124	15	US-10-121-464-14	Sequence 14, Appl
41	468.5	71.5	249	11	US-09-880-748-1730	Sequence 1730, Ap
42	468	71.5	248	11	US-09-880-748-1178	Sequence 1178, Ap
43	467.5	71.4	245	11	US-09-880-748-1919	Sequence 1919, Ap
44	467	71.3	142	15	US-10-171-452A-2	Sequence 2, Appli
45	466.5	71.2	126	11	US-09-791-153A-62	Sequence 62, Appl

ALIGNMENTS

```
RESULT 1
US-10-056-794-19
; Sequence 19, Application US/10056794
; Publication No. US2003011907841
GENERAL INFORMATION:
   APPLICANT:  Graves, Scott S.
               Reno, John M.
               Mallett, Robert W.
               Hylarides, Mark D.
               Searle, Stephen M.J.
               Henry, Andrew H.
               Pedersen, Jan T.
               Rees, Anthony R.
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE
                    ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN
                    PRETARGETING METHODS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
   ADDRESSEE: Seed IP Law Group
   STREET: 701 Fifth Avenue, Suite 6300
   CITY: Seattle
   STATE: Washington
   COUNTRY: USA
   ZIP: 98104
COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/10/056,794
   FILING DATE: 24-Jan-2002
   CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
   NAME: Sharkey Ph.D., Richard G.
   REGISTRATION NUMBER: 32,629
   REFERENCE/DOCKET NUMBER: 690022.527C2
TELECOMMUNICATION INFORMATION:
```

```
                TELEPHONE: (206) 622-4900
                TELEFAX: (206) 682-6031
      INFORMATION FOR SEQ ID NO: 19:
          SEQUENCE CHARACTERISTICS:
                LENGTH: 120 amino acids
                TYPE: amino acid
                STRANDEDNESS: <Unknown>
                TOPOLOGY: linear
          SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-056-794-19

Query Match      79.9%;    Score 523.5;   DB 15;   Length 120;
Best Local Similarity   82.9%;    Pred. No. 1.6e-45;
Matches 102;  Conservative    8;  Mismatches 10;  Indels    3;  Gaps    1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||||||||||||| :||||||||| |:|||||||| ||
Db    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYMHWVRQAPGQLQWMGRIDPANGNTKC 60

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYNYGVYAMDYWGQGTLVT 120
          | ||||||||||||| :||||||||||||| :||   | ::||||||||||
Db   61 DLSFQGRVTITADTSINTAYMELSSLRSDDTAVYYCSREVL---TGTWSLDYWGQGTLVT 117

Qy  121 VSS 123
          |||
Db  118 VSS 120
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RESULT 2
US-10-244-821-4
; Sequence 4, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence for huNR-LU-10
; OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
US-10-244-821-4

```
Query Match      79.9%;    Score 523.5;   DB 12;   Length 431;
Best Local Similarity   82.9%;    Pred. No. 7e-45;
Matches 102;  Conservative    8;  Mismatches 10;  Indels    3;  Gaps    1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||||||||||||| :||||||||| |:|||||||| ||
Db  148 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYMHWVRQAPGQLQWMGRIDPANGNTKS 207

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYNYGVYAMDYWGQGTLVT 120
          | ||||||||||||| :||||||||||||| :||   | ::||||||||||
Db  208 DLSFQGRVTITADTSINTAYMELSSLRSDDTAVYYCSREVL---TGTWSLDYWGQGTLVT 264

Qy  121 VSS 123
          |||
Db  265 VSS 267
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RESULT 3
US-10-013-173-4
; Sequence 4, Application US/10013173
; Publication NO. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence for huNR-LU-10
; OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
US-10-013-173-4

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Query Match      79.9%;    Score 523.5;   DB 15;   Length 431;
Best Local Similarity   82.9%;    Pred. No. 7e-45;
Matches 102;  Conservative    8;  Mismatches 10;  Indels    3;  Gaps    1;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||||||||||||||||||||||||||||||||| :||||||||| |:|||||||| ||
Db  148 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYMHWVRQAPGQLQWMGRIDPANGNTKS 207

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYNYGVYAMDYWGQGTLVT 120
          | ||||||||||||| :||||||||||||| :||   | ::||||||||||
Db  208 DLSFQGRVTITADTSINTAYMELSSLRSDDTAVYYCSREVL---TGTWSLDYWGQGTLVT 264

Qy  121 VSS 123
          |||
Db  265 VSS 267
```

RESULT 4
US-10-150-762-4
; Sequence 4, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150,762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence for huNR-LU-10
; OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
US-10-150-762-4

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Query Match      79.9%;    Score 523.5;   DB 15;   Length 431;
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              GenCore version 5.1.6
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October 7, 2003, 09:09:40 ; Search time 17.3939 Seconds
                                        (without alignments)
                                        680.050 Million cell updates/sec

Title:         US-09-155-739-11
Perfect score: 655
Sequence:      1 QVQLVQSGAEVKKPGASVKV.........NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters:    283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_76:*
             1: pir1:*
             2: pir2:*
             3: pir3:*
             4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                    SUMMARIES
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Result No.	Score	Query Match %	Length	DB	ID	Description
1	488.5	74.6	178	2	S29594	Ig gamma chain (WM
2	477	72.8	120	2	S03471	Ig heavy chain V-D
3	473.5	72.3	118	2	S36265	Ig heavy chain V-1
4	468	71.5	123	2	D33548	Ig heavy chain V-1
5	467	71.3	142	2	A32483	Ig heavy chain V r
6	465	71.0	117	2	S17586	Ig heavy chain V r
7	459.5	70.2	122	2	S06823	Ig heavy chain V r
8	456.5	69.7	132	2	PH0954	Ig heavy chain V r
9	455	69.5	116	2	S24289	Ig gamma chain V r
10	455	69.5	221	2	S49220	Ig gamma-1 chain -
11	450	68.7	129	2	S46393	Ig heavy chain V r
12	449	68.5	115	2	S03482	Ig heavy chain V-D
13	447.5	68.3	135	2	S49530	anti-Sm antibody V
14	447	68.2	120	2	S03484	Ig heavy chain V-D
15	446.5	68.2	136	2	PH0960	Ig heavy chain V r
16	444	67.8	136	2	S04576	Ig heavy chain pre
17	443	67.6	119	2	PH0961	Ig heavy chain V r
18	441.5	67.4	268	2	A56446	Ig heavy chain V r
19	439.5	67.1	104	2	PH1665	Ig heavy chain V r
20	439.5	67.1	114	2	A47271	nitrophenyl phosph
21	439	67.0	133	2	C33548	Ig heavy chain V-1
22	439	67.0	627	2	S14683	Ig mu chain precur
23	438.5	66.9	114	2	PH1667	Ig heavy chain V r
24	438.5	66.9	118	2	PH1666	Ig heavy chain V r
25	437.5	66.8	137	2	S52445	Ig heavy chain V r
26	436.5	66.6	120	2	S31999	Ig heavy chain V r
27	435.5	66.5	120	2	PH0962	Ig heavy chain V r
28	435.5	66.5	128	2	PH0952	Ig heavy chain V-1
29	433.5	66.2	126	2	B33548	Ig heavy chain V-1
30	433	66.1	127	2	PH0955	Ig heavy chain V r
31	433	66.1	135	2	PH0953	Ig heavy chain V r
32	431	65.8	126	2	I44151	Ig heavy chain V r
33	429.5	65.6	108	2	PH1012	Ig heavy chain V r
34	429	65.5	125	2	PH0957	Ig heavy chain pre
35	427.5	65.3	143	1	E1HUND	Ig heavy chain V r
36	427	65.2	125	2	S68170	Ig heavy chain V-1
37	427	65.2	127	2	A33548	Ig heavy chain V-1
38	426	65.0	127	2	S34014	Ig heavy chain V r
39	425	64.9	129	2	S36260	Ig heavy chain V r
40	424.5	64.8	147	2	PH1561	Ig heavy chain V r
41	424.5	64.8	171	2	S23523	Ig heavy chain V r
42	421	64.3	246	2	S38950	Ig gamma chain - m
43	421	64.3	446	2	S40295	Ig gamma-2a chain
44	420.5	64.2	122	2	PH1426	Ig heavy chain V r
45	420	64.1	121	2	S20783	Ig heavy chain V r

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                    ALIGNMENTS

RESULT 1
S29594
Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
R;Seymour, R.
submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29594
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <SEY>
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin

Query Match            74.6%;   Score 488.5;  DB 2;   Length 178;
Best Local Similarity  75.6%;   Pred. No. 1.1e-36;
Matches   93; Conservative  11; Mismatches  14; Indels   5; Gaps   2;

Qy    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYIHWRQAPGQRLEWMGRIDPANGYTKY 60
          :||| ||||| ||||||:|| |||||||||||||:||:| | |||:|||||||||||||:|
Db   14 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRIDPANGYTEY 73

Qy   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYIGNYGVYAMDYWGQGTLVT 120
          |||||| ||||||| |||:|| ||||||||||||||:| ||| ::|||||||||||| ||
Db   74 DPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG----GNY-AYGMDYWGQGTSVT 128

Qy  121 VSS 123
          |||
Db  129 VSS 131

RESULT 2
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03471
A;Molecule type: mRNA
A;Residues: 7-120 <ROC1>
A;Cross-references: EMBL:X01820; NID:g51820; PIDN:CAA25962.1; PID:g133983
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
```

A;Reference number: S07453; MUID:83058021; PMID:6815271
A;Accession: S07453
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match    72.8%;   Score 477;  DB 2;  Length 120;
Best Local Similarity  75.6%;   Pred. No. 8e-36;
   Matches  93;  Conservative  11;  Mismatches  15;  Indels  4;  Gaps  1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         ||||||||||| ||||||||| ||||||||||||||:||||:::||||| |||
Db   1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
         ||||||::||||||::|:||:||||||||||||||| |   ||||||| |
Db  61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR---GWLRRDAMDYWGQGTSVT 116

Qy 121 VSS 123
         |||
Db 117 VSS 119
```

RESULT 3
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 23-Jul-1999
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36265
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GRI>
A;Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match    72.3%;   Score 473.5;  DB 2;  Length 118;
Best Local Similarity  76.2%;   Pred. No. 1.6e-35;
   Matches  96;  Conservative  6;  Mismatches  13;  Indels  11;  Gaps  2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         ||||||||||||||||||||||||||    :||||||::|:| |
Db   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE--GYYGNYGVYAMDYWGQGT 117
         ||||||:||||||||||||||||||||||||||||||   :||
Db  61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSGY------LDYWGQGT 112

Qy 118 LVTVSS 123
         ||||||
Db 113 LVTVSS 118
```

RESULT 4
D33548
Ig heavy chain V-I region (WIL2) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: D33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: D33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Molecule type: mRNA
A;Residues: 1-123 <KIP>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match    71.5%;   Score 468;  DB 2;  Length 123;
Best Local Similarity  74.8%;   Pred. No. 5.2e-35;
   Matches  92;  Conservative  7;  Mismatches  24;  Indels  0;  Gaps  0;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         |||||||||||||||||||||::||:::||::|:::|::||:::::::|::::::
Db   1 QVQLVQSGAEVKKPGASVKVSCEASGYTFTGYMHWHVRQAPGQGLEWMGWINPNSGGTNY 60

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGTLVT 120
         ||||||||| :|||: :||:||||| ||:||||||||:      ||||||||||
Db  61 AEKFQGRVTITRDTSINTAYMELSRLRSDDTAVYYCARASYCGYDCYYFPDYWGQGTLVT 120

Qy 121 VSS 123
         ||
Db 121 VSS 123
```

RESULT 5
A32483
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C;Accession: A32483
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells
A;Reference number: A32483; MUID:89273586; PMID:2499327
A;Accession: A32483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-142 <LAR>
A;Cross-references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>

```
Query Match    71.3%;   Score 467;  DB 2;  Length 142;
Best Local Similarity  73.2%;   Pred. No. 7.5e-35;
   Matches  93;  Conservative  8;  Mismatches  22;  Indels  4;  Gaps  1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
         ||||||||||||||||||||||||:||::::|::||||||:::::||::::::::||
Db  11 QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYMHWVRQAPGQGLEWMGIINPSGSNTNY 70

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE---GYYGNYGVYAMDYWGQG 116
         ||||||:|| ::|:::|||||||||||||||||||||    :|||||||||
Db  71 AQKFQGRVTMRDTSTSTVYMELSSLRSEDTAVYYCAREKLATTIFGVLIITGMDYWGQG 130

Qy 117 TLVTVSS 123
         |||||||
Db 131 TLVTVSS 137
```

RESULT 6
S17586
Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S17586
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
forms.
A;Reference number: S17586; MUID:92015240; PMID:1656053
A;Accession: S17586
A;Status: preliminary
A;Molecule type: mRNA

```
                    GenCore version 5.1.6
              Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October 7, 2003, 09:02:30 ; Search time 9.19394 Seconds
                                        (without alignments)
                             629.141 Million cell updates/sec

Title:       US-09-155-739-11
Perfect score: 655
Sequence:    1 QVQLVQSGAEVKKPGASVKV.........NYGVYAMDYWGQGTLVTVSS 123

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:  127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:        127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  SwissProt_41:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	427.5	65.3	147	1	HV1C_HUMAN	P01744 homo sapien
2	409	62.4	120	1	HV03_MOUSE	P01747 mus musculu
3	408.5	62.4	139	1	HV07_MOUSE	P01751 mus musculu
4	405	61.8	140	1	HV1B_HUMAN	P01743 homo sapien
5	399	60.9	140	1	HV02_MOUSE	P01746 mus musculu
6	396	60.5	117	1	HV1G_HUMAN	P23083 homo sapien
7	390	59.5	117	1	HV1A_HUMAN	P01742 homo sapien
8	378	57.7	117	1	HV13_MOUSE	P01757 mus musculu
9	375.5	57.3	118	1	HV51_MOUSE	P06330 mus musculu
10	373	56.9	117	1	HV12_MOUSE	P01756 mus musculu
11	371.5	56.7	137	1	HV11_MOUSE	P01755 mus musculu
12	369	56.3	138	1	HV48_MOUSE	P03980 mus musculu
13	364.5	55.6	120	1	HV50_MOUSE	P06329 mus musculu
14	360	55.0	121	1	HV01_MOUSE	P01745 mus musculu
15	360	55.0	136	1	HV15_MOUSE	P01759 mus musculu
16	355	54.2	125	1	HV1F_HUMAN	P06326 homo sapien
17	349.5	53.4	120	1	HV1H_HUMAN	P80421 homo sapien
18	349	53.3	117	1	HV09_MOUSE	P01753 mus musculu
19	344.5	52.6	114	1	HV00_MOUSE	P01741 mus musculu
20	338	51.6	117	1	HV04_MOUSE	P01748 mus musculu
21	336	51.3	117	1	HV06_MOUSE	P01750 mus musculu
22	333.5	50.9	136	1	HV16_MOUSE	P01783 mus musculu
23	333	50.8	117	1	HV10_MOUSE	P01754 mus musculu
24	330.5	50.5	124	1	HV1E_HUMAN	P01761 homo sapien
25	329	50.2	117	1	HV14_MOUSE	P01758 mus musculu
26	329	50.2	117	1	HV49_MOUSE	P06328 mus musculu
27	326	49.8	117	1	HV52_MOUSE	P06327 mus musculu
28	326	49.8	123	1	HV24_MOUSE	P01793 mus musculu
29	325.5	49.7	119	1	HV37_HUMAN	P01807 homo sapien
30	325.5	49.7	124	1	HV1D_MOUSE	P01760 homo sapien
31	324.5	49.5	119	1	HV38_MOUSE	P01808 mus musculu
32	323.5	49.4	119	1	HV40_MOUSE	P01810 mus musculu
33	320.5	48.9	122	1	HV3G_HUMAN	P01768 homo sapien
34	319	48.7	117	1	HV42_MOUSE	P01812 mus musculu
35	318.5	48.6	122	1	HV3A_HUMAN	P01762 homo sapien
36	318	48.5	121	1	HV3J_HUMAN	P01771 homo sapien
37	317	48.4	123	1	HV19_MOUSE	P01788 mus musculu
38	315	48.1	123	1	HV18_MOUSE	P01787 mus musculu
39	314.5	48.0	122	1	HV21_MOUSE	P01790 mus musculu
40	314	47.9	117	1	HV05_MOUSE	P01749 mus musculu
41	313	47.8	123	1	HV25_MOUSE	P01794 mus musculu
42	313	47.8	142	1	HV01_RAT	P01805 rattus norv
43	312	47.6	118	1	HV39_MOUSE	P01809 mus musculu
44	312	47.6	123	1	HV22_MOUSE	P01791 mus musculu
45	311.5	47.6	122	1	HV3H_HUMAN	P01769 homo sapien

ALIGNMENTS

```
RESULT 1
HV1C_HUMAN
ID   HV1C_HUMAN    STANDARD;     PRT;    147 AA.
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-I region ND precursor (Fragments).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83065234; PubMed=6815656;
RA   Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA   Bell L.O., Gould H.J.;
RT   "Cloning and sequence determination of the gene for the human
RT   immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN   [2]
RP   SEQUENCE OF 20-147.
RA   Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL   (In) Bach M.K. (eds.);
RL   Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL   Marcel Dekker, New York (1978).
CC   -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01789; 1MCP.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     19
FT   CHAIN        20    147       IG HEAVY CHAIN V-I REGION ND.
FT   DOMAIN       20    131       IG-LIKE.
FT   MOD_RES      20     20       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     41    115
FT   CONFLICT     21     21       T -> V (IN REF. 2).
FT   CONFLICT     53     54       IH -> HI (IN REF. 2).
FT   CONFLICT     67     68       VG -> GV (IN REF. 2).
FT   CONFLICT    125    125       MISSING (IN REF. 2).
FT   NON_TER     147    147
SQ   SEQUENCE   147 AA;   16491 MW;  948F9F72A5366C20 CRC64;

Query Match             65.3%;  Score 427.5;  DB 1;  Length 147;
Best Local Similarity   64.1%;  Pred. No. 1.1e-36;
Matches   82;  Conservative   16;  Mismatches   25;  Indels    5;  Gaps    1;
```

```
Qy    1 QYQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          | :||||||||:||||:|||||:||||||:     |:|||||||| |||: :|| |
Db   20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY 79

Qy   61 DPKFQQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-----EGYYGNYGVYAMDYWGQ 115
          :|||:|||| | | |||||:|  | ||:||:||||||:       || ||| ||  :|||
Db   80 APRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNFDYSYTLDVWGQ 139

Qy  116 GTLVTVSS 123
          || ||||
Db  140 GTTVTVSS 147
```

RESULT 2
HV03_MOUSE
ID   HV03_MOUSE   STANDARD;   PRT;   120 AA.
AC   P01747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83131846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
CC   -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC   DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC   CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC   SEGMENT, JH2.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Hybridoma.
FT   DOMAIN   1   111   IG-LIKE.
FT   NON_TER   120   120
SQ   SEQUENCE   120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match   62.4%; Score 409; DB 1; Length 120;
Best Local Similarity   63.1%; Pred. No. 6.5e-35;
Matches   77; Conservative 18; Mismatches 25; Indels 2; Gaps 1;

```
Qy    2 VQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD 61
          ||| |||||:|:|||||:|||||:|||:|:||| :|:||:|:|||||| |:| |||||||:
Db    1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN 60

Qy   62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVTV 121
          ||||||:| | |:||||||| || |: :|||||||:|  :|||||||  |:|||||||:||
Db   61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYG--GSYYFDYWGQGTLITV 118

Qy  122 SS 123
          ||
Db  119 SS 120
```

RESULT 3
HV07_MOUSE
ID   HV07_MOUSE   STANDARD;   PRT;   139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region B1-8/186-2 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC   MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC   (NPB ANTIBODIES).
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A90809; MHMS18.
DR   PDB; 1A6U; 27-MAY-98.
DR   PDB; 1A6W; 15-JUL-98.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; 3D-structure.
FT   SIGNAL   1   19
FT   CHAIN   20   139   IG HEAVY CHAIN V REGION B1-8/186-2.
FT   DOMAIN   20   49   FRAMEWORK-1.
FT   DOMAIN   50   54   COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN   55   68   FRAMEWORK-2.
FT   DOMAIN   69   85   COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN   86   117   FRAMEWORK-3.
FT   DOMAIN   118   124   D SEGMENT.
FT   DOMAIN   125   139   JH2 SEGMENT.
FT   DISULFID   41   115   BY SIMILARITY.
FT   NON_TER   139   139
SQ   SEQUENCE   139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match   62.4%; Score 408.5; DB 1; Length 139;
Best Local Similarity   62.6%; Pred. No. 8.6e-35;
Matches   77; Conservative 18; Mismatches 25; Indels 3; Gaps 1;

```
Qy    1 QYQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||:| ||| ::||:||||:| ||||:|||||:|:|: |:|||:: ||||:|:| ||||
Db   20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79

Qy   61 DPKFQQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |:| |:|||:|| ||:|||::|||||:|||||||  | |:|  :|:: ::|:|| || :|
Db   80 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARYDYYGS---SYFDYWGQGTTLT 136

Qy  121 VSS 123
          |||
Db  137 VSS 139
```

RESULT 4
HV1B_HUMAN
ID   HV1B_HUMAN   STANDARD;   PRT;   117 AA.
AC   P01743;
DT   21-JUL-1986 (Rel. 01, Created)

```
                 GenCore version 5.1.6
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October 7, 2003, 09:09:15 ; Search time 43.9818 Seconds
                                        (without alignments)
                                        721.673 Million cell updates/sec

Title:            US-09-155-739-11
Perfect score:    655
Sequence:         1 QVQLVQSGAEVKKPGASVKV.........NYGVYAMDYWGQGTLVTVSS 123

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:    830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SPTREMBL_23:*
                 1: sp_archea:*
                 2: sp_bacteria:*
                 3: sp_fungi:*
                 4: sp_human:*
                 5: sp_invertebrate:*
                 6: sp_mammal:*
                 7: sp_mhc:*
                 8: sp_organelle:*
                 9: sp_phage:*
                 10: sp_plant:*
                 11: sp_rodent:*
                 12: sp_virus:*
                 13: sp_vertebrate:*
                 14: sp_unclassified:*
                 15: sp_rvirus:*
                 16: sp_bacteriap:*
                 17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	457.5	69.8	124	4	Q9UL92	Q9UL92 homo sapien
2	440.5	67.3	159	4	Q96QS0	Q96QS0 homo sapien
3	440	67.2	468	11	Q99L31	Q99l31 mus musculu
4	432	66.0	109	11	Q9JL85	Q9JL85 mus musculu
5	432	66.0	119	4	Q9UL94	Q9UL94 homo sapien
6	432	66.0	614	4	Q96GA6	Q96GA6 homo sapien
7	428	65.3	119	5	Q9GYZ2	Q9GYZ2 schistosoma
8	428	65.3	125	4	Q9UL95	Q9UL95 homo sapien
9	427	65.2	146	11	Q924Q3	Q924q3 mus musculu
10	422	64.4	473	11	Q9DBL4	Q9d8l4 mus musculu
11	415.5	63.4	145	11	Q924R1	Q924r1 mus musculu
12	415.5	63.4	145	11	Q924R4	Q924r4 mus musculu
13	414.5	63.3	482	11	Q8K172	Q8K172 mus musculu
14	412	62.9	146	11	Q924R8	Q924r8 mus musculu
15	411.5	62.8	116	4	Q9UL89	Q9UL89 homo sapien
16	409.5	62.5	145	11	Q924Q6	Q924q6 mus musculu
17	408.5	62.4	145	11	Q924Q7	Q924q7 mus musculu
18	408.5	62.4	473	11	Q99L25	Q99l25 mus musculu
19	408	62.3	142	11	Q924Q1	Q924q1 mus musculu
20	407.5	62.2	143	11	Q924P9	Q924p9 mus musculu
21	407	62.1	117	11	Q9QXE9	Q9qxe9 mus musculu
22	405.5	61.9	145	11	Q924Q9	Q924q9 mus musculu
23	405	61.8	140	11	Q924R2	Q924r2 mus musculu
24	403.5	61.6	143	11	Q924R0	Q924r0 mus musculu
25	403.5	61.6	145	11	Q924P7	Q924p7 mus musculu
26	403.5	61.6	488	11	Q8K0F2	Q8K0F2 mus musculu
27	399	60.9	142	11	Q924Q2	Q924q2 mus musculu
28	399	60.9	150	4	Q9Y298	Q9y298 homo sapien
29	398.5	60.8	500	4	Q9BRV0	Q9brv0 homo sapien
30	398	60.8	481	11	Q91WT1	Q91wt1 mus musculu
31	394.5	60.2	143	11	Q924R7	Q924r7 mus musculu
32	393.5	60.1	145	11	Q924R3	Q924r3 mus musculu
33	391.5	59.8	488	11	Q91WR1	Q91wr1 mus musculu
34	389.5	59.5	137	11	Q924R6	Q924r6 mus musculu
35	389.5	59.5	143	11	Q91VA2	Q91va2 mus musculu
36	388.5	59.3	139	11	Q924R5	Q924r5 mus musculu
37	388.5	59.3	141	11	Q924Q4	Q924q4 mus musculu
38	386.5	59.0	118	11	Q921C4	Q921c4 mus musculu
39	386	58.9	117	11	Q9QXF0	Q9qxf0 mus musculu
40	384	58.6	157	4	O95978	O95978 homo sapien
41	383.5	58.5	613	11	Q8VCX7	Q8vcx7 mus musculu
42	381.5	58.2	143	11	Q91V67	Q91v67 mus musculu
43	381.5	58.2	463	11	Q99LC4	Q99lc4 mus musculu
44	381	58.2	146	11	Q924Q8	Q924q8 mus musculu
45	380.5	58.1	143	11	Q924Q5	Q924q5 mus musculu

ALIGNMENTS

```
RESULT 1
Q9UL92
ID   Q9UL92       PRELIMINARY;      PRT;    124 AA.
AC   Q9UL92;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035022; AAD56258.1; -.
     HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER        1
FT   NON_TER        124
SQ   SEQUENCE   124 AA;   13580 MW;  1BAAACBD96ACD2A2 CRC64;

Query Match             69.8%;     Score 457.5;   DB 4;   Length 124;
Best Local Similarity   69.5%;     Pred. No. 7.3e-41;
Matches   91;  Conservative   9;  Mismatches  16;  Indels  15;  Gaps    2;

Qy        1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY  60
            :||||:||||||||||||||||||||||||||  |||||| |||||| |:|:| |:: |||  |
```

```
Db   1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAM------DY 112
        |||||||:|  ||| ||  ||||||||||||||||||||      ||  ::  ||
Db  61 AQKFQGRVTMTRDFSTSTVYMELSSLRSEDTAVYYCAR------GLYVVVPAAFSRFDY 113

Qy 113 WGQGTLVTVSS 123
        |||||||||||
Db 114 WGQGTLVTVSS 124

RESULT 2
Q96QS0
ID   Q96QS0        PRELIMINARY;    PRT;    159 AA.
AC   Q96QS0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Putative matrix cell adhesion molecule-3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tilson M.D.;
RT   "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RT   mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY039025; AAK82649.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match             67.3%;  Score 440.5; DB 4; Length 159;
Best Local Similarity   64.9%;  Pred. No. 6.4e-39;
Matches   87; Conservative  13; Mismatches  19; Indels  15; Gaps  2;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        ||||||||||||||||||||||||||::  : :||||||||  || |:| :|
Db  20 QVQLVQSGAELVRPGASVKLSCTASGYTFSNYMNWVRQAPGQGPEWMGVINPSGGSARY 79

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE----------GYYGNYGVYA 109
        |||||:|:| ||| |: |||||||||||||||||||||       :|  !
Db  80 SQKFQGRLTMTRDTSTSTVYMDLSSLRSDDTAVYFCAREMEITFGGAVSKGFY----YYG 135

Qy 110 MDYWGQGTLVTVSS 123
        |:  |||||||||
Db 136 MDVWGQGTTVTVSS 149

RESULT 3
Q99L31
ID   Q99L31        PRELIMINARY;    PRT;    468 AA.
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to RIKEN cDNA 1810060009 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
DR   HSSP; P01842; 7FAB.
```

```
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE 468 AA; 51661 MW; 9635232B3332ADB CRC64;

Query Match             67.2%;  Score 440; DB 11; Length 468;
Best Local Similarity   67.5%;  Pred. No. 2.8e-38;
Matches   83; Conservative  16; Mismatches  20; Indels  4; Gaps  1;

Qy   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
        :|||||||||: :||||: :|||||||||: | ||: : || |: : ||| :|||
Db  20 EVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRPEQGLEWIGWIDPEDGETKY 79

Qy  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
        |||| : ||||||||||||||||||||||||||: ||||||       |||:|
Db  80 APKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCARNLLYGGY----YDYWGQGTTT 135

Qy 121 VSS 123
        |||
Db 136 VSS 138

RESULT 4
Q9JL85
ID   Q9JL85        PRELIMINARY;    PRT;    109 AA.
AC   Q9JL85;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Anti-myosin immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=20448942; PubMed=10992488;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-Cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206021; AAF69319.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1       1
FT   NON_TER     109     109
SQ   SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match             66.0%;  Score 432; DB 11; Length 109;
Best Local Similarity   68.7%;  Pred. No. 3.2e-38;
Matches   79; Conservative  15; Mismatches  15; Indels  6; Gaps  1;

Qy   9 AEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYDPKFQGRV 68
        |:: |||||||||||:|||||:|||||||||||||||||||: |:|||||||||||||
Db   1 AELVKPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA 60

Qy  69 TITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVTVSS 123
        |||||||::||::|||||||||||||:||||     :|||||:|||||||||
Db  61 TITSDTSNTAYLQLSSLTSEDTAVYYCVRR------GAVFDYWGQGTALTVSS 109
```

OM protein - protein search, using sw model

```
                        GenCore version 5.1.6
            Copyright (C) 1993 - 2003 Compugen Ltd.
```

Run on: October 7, 2003, 09:01:50 ; Search time 54.9818 seconds
                                           (without alignments)
                                           363.748 Million cell updates/sec

Title: US-09-155-739-2
Perfect score: 680
Sequence: 1 MRPSIQFLGLLLFWLHGAQC.........YCLQYDNLWTFGGGTKLEIK 126

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_19Jun03:*
            1: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1980.DAT:*
            2: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1981.DAT:*
            3: /SIDS1/gcgdata/geneseq/geneseq-embl/AA1982.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 680 | 100.0 | 126 | 16 | AAR81326 | Mouse VLA-4 antibo |
| 2 | 680 | 100.0 | 126 | 16 | AAR81332 | Human VLA-4 reshap |
| 3 | 680 | 100.0 | 126 | 18 | AAW22409 | Alpha-4 integrin m |
| 4 | 634 | 93.2 | 128 | 15 | AAR60627 | ME1-14 light chain |
| 5 | 619 | 91.0 | 126 | 18 | AAW22419 | Humanised alpha-4 |
| 6 | 618.5 | 91.0 | 128 | 11 | AAR06252 | Variable region of |
| 7 | 569 | 83.7 | 106 | 16 | AAR81328 | Mouse anti-VLA-4 a |
| 8 | 539 | 79.3 | 359 | 20 | AAY29913 | Human MCP-3 and mu |
| 9 | 539 | 79.3 | 361 | 20 | AAY29911 | Human IP-10 and mu |
| 10 | 535 | 78.7 | 374 | 20 | AAY29916 | Artificial synthet |
| 11 | 510.5 | 75.1 | 107 | 16 | AAR78970 | Light chain variab |
| 12 | 508 | 74.7 | 106 | 16 | AAR81321 | Humanised anti-VLA |
| 13 | 508 | 74.7 | 106 | 18 | AAW22412 | Humanised alpha-4 |
| 14 | 508 | 74.7 | 108 | 17 | AAR93159 | Murine monoclonal |
| 15 | 508 | 74.7 | 637 | 13 | AAR26983 | (FRP51)-ETA fusion |
| 16 | 507 | 74.6 | 245 | 19 | AAW26800 | Anti-gp54 MAb T16 |
| 17 | 503 | 74.0 | 109 | 19 | AAW26797 | Anti-gp54 MAb T16 |
| 18 | 503 | 74.0 | 240 | 16 | AAR85495 | ScFv(FWP51). Synt |
| 19 | 501 | 73.7 | 355 | 18 | AAW35133 | R. pipiens recombi |
| 20 | 500 | 73.5 | 109 | 12 | AAR13658 | Murine OKT4A light |
| 21 | 500 | 73.5 | 241 | 13 | AAR26981 | FWP51 fusion prote |
| 22 | 479.5 | 70.5 | 234 | 12 | AAR13050 | CD4-specific CDR-g |
| 23 | 464.5 | 68.3 | 128 | 22 | AAB81995 | Ganglioside GD3 sp |
| 24 | 462.5 | 68.0 | 234 | 18 | AAW10233 | TF8-5G9 CDR-grafte |
| 25 | 458.5 | 67.4 | 260 | 23 | ABP41164 | Human ovarian anti |
| 26 | 457.5 | 67.3 | 128 | 22 | AAB81996 | Ganglioside GD3 sp |
| 27 | 456.5 | 67.1 | 129 | 15 | AAR57482 | Humanised 1308F VL |
| 28 | 456.5 | 67.1 | 129 | 17 | AAR92085 | Humanised antibody |
| 29 | 456.5 | 67.1 | 129 | 23 | ABG31444 | Amino acid sequenc |
| 30 | 455.5 | 67.0 | 129 | 15 | AAR47207 | Human/murine IL-1 |
| 31 | 452.5 | 66.5 | 128 | 22 | AAB81997 | Ganglioside GD3 sp |
| 32 | 451.5 | 66.4 | 127 | 12 | AAR12359 | Light (kappa) chai |
| 33 | 451.5 | 66.4 | 129 | 21 | AAY56724 | Amino acid sequenc |
| 34 | 448.5 | 66.0 | 128 | 22 | AAB81993 | Ganglioside GD3 sp |
| 35 | 447.5 | 65.8 | 129 | 19 | AAW70379 | Anti-human CD23 5E |
| 36 | 446.5 | 65.7 | 126 | 12 | AAR12237 | Mouse MAb 1C11 L c |
| 37 | 446.5 | 65.7 | 129 | 14 | AAR30880 | pXOM2. Mus muscul |
| 38 | 445.5 | 65.5 | 132 | 18 | AAW22842 | Human anti-tumour |
| 39 | 443.5 | 65.2 | 130 | 21 | AAY56737 | Amino acid sequenc |
| 40 | 442.5 | 65.1 | 236 | 23 | AAU74297 | Anti-human AILIM m |
| 41 | 442 | 65.0 | 124 | 21 | AAY56719 | Amino acid sequenc |
| 42 | 441 | 64.9 | 237 | 21 | AAY96301 | Human IGFAM-13 imm |
| 43 | 441 | 64.8 | 241 | 22 | AAB82912 | Human immune respo |
| 44 | 440.5 | 64.8 | 129 | 23 | ABG97823 | Human HEF-12B5H-g |
| 45 | 440.5 | 64.8 | 129 | 23 | ABG35326 | Thrombopoietin ago |

ALIGNMENTS

```
RESULT 1
AAR81326
ID   AAR81326 standard; Protein; 126 AA.
XX
AC   AAR81326;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "signal peptide"
FT   Region          21..43
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /note= "framework region 4"
```

```
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;  95WO-US01219.
XX
PR   25-JAN-1994;  94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99889.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 1; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 light chain variable
CC   region directed against leukocyte adhesion molecule VLA-4.  Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence  126 AA;

Query Match          100.0%;  Score 680;  DB 16;  Length 126;
Best Local Similarity 100.0%;  Pred. No. 2.3e-47;
Matches 126;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60

Qy  61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120

Qy 121 TKLEIK 126
        ||||||
Db 121 TKLEIK 126

RESULT 2
AAR81332
ID   AAR81332 standard; Protein; 126 AA.
XX
AC   AAR81332;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
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OS   Homo sapiens.
XX
FH   Key        Location/Qualifiers
FT   Peptide    1..20
FT              /note= "signal peptide"
FT   Region     21..43
FT              /note= "framework region 1"
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FT   Region     55..69
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FT   Region     77..108
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FT              /note= "complementarity determining region 3"
FT   Region     117..126
FT              /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;  95WO-US01219.
XX
PR   25-JAN-1994;  94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99893.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 10; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 light
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4.  The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (See AAQ99895-98) and
CC   then subcloned into mammalian cell expression vectors containing
CC   human kappa or gamma-1 constant regions.  In the humanized light
CC   chain, amino acids L45, L49, L58 and L69  in the human kappa LC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain.  Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells.  The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as
CC   multiple sclerosis.  They can also be used in the treatment of
CC   stroke, cerebral traumas, meningitis or encephalitis.  The
CC   antibodies can also be used for detecting VLA-4, for affinity
CC   purification or for generating anti-idiotype antibodies.
XX
SQ   Sequence  126 AA;

Query Match          100.0%;  Score 680;  DB 16;  Length 126;
Best Local Similarity 100.0%;  Pred. No. 2.3e-47;
Matches 126;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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        Copyright (c) 1993 - 2003 Compugen Ltd.
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Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 328717 segs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
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2	680	100.0	126	2	US-08-561-521-15	Sequence 15, Appl
3	680	100.0	126	2	PCT-US95-01219-2	Sequence 2, Appl
4	680	100.0	126	5	PCT-US95-01219-15	Sequence 15, Appl
5	634	93.2	128	1	US-08-339-582-4	Sequence 4, Appli
6	569	83.7	106	2	US-08-561-521-5	Sequence 5, Appli
7	569	83.7	106	5	PCT-US95-01219-5	Sequence 5, Appli
8	539	79.3	359	4	US-09-646-028-16	Sequence 16, Appl
9	539	79.3	361	4	US-09-646-028-13	Sequence 13, Appl
10	535	78.7	374	4	US-09-646-028-15	Sequence 15, Appl
11	510.5	75.1	107	2	US-08-888-366-22	Sequence 22, Appl
12	508	74.7	106	2	US-08-561-521-7	Sequence 7, Appli
13	508	74.7	106	5	PCT-US95-01219-7	Sequence 7, Appli
14	508	74.7	637	16	US-08-235-838-16	Sequence 16, Appl
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16	503	74.0	241	1	US-08-235-838-11	Sequence 11, Appl
17	503	74.0	241	1	US-08-465-473B-11	Sequence 11, Appl
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25	437.5	64.3	131	5	PCT-US95-05262-2	Sequence 2, Appli
26	435.5	64.0	234	4	US-09-740-002-24	Sequence 24, Appl
27	434.5	63.9	128	4	US-09-225-322B-10	Sequence 10, Appl
28	434.5	63.9	128	4	US-09-225-322B-19	Sequence 19, Appl
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45	416.5	61.3	127	2	US-08-621-751A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-561-521-2
; Sequence 2, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-2

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Best Local Similarity 100.0%; Pred. No. 2.1e-59;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  121 TKLEIK 126
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; Sequence 2, Application PCT/US9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 126 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US95-01219-2

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Best Local Similarity 100.0%;   Pred. No. 2.1e-59;
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; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran

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RESULT 2
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; Sequence 15, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/561,521
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/186,269A
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 15:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 126 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-15

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

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Post-processing:  Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	539	79.3	361	12	US-10-335-394-13	Sequence 13, Appl
3	535	78.7	374	12	US-10-335-394-15	Sequence 15, Appl
4	490	72.1	109	9	US-09-229-200A-7	Sequence 7, Appl
5	482.5	71.0	108	9	US-09-229-200A-17	Sequence 17, Appl
6	481.5	70.8	131	15	US-10-207-655-256	Sequence 256, App
7	481.5	70.8	266	15	US-10-207-655-260	Sequence 260, App
8	481.5	70.8	550	15	US-10-207-655-270	Sequence 270, App
9	445.5	65.5	127	12	US-10-268-883-5	Sequence 5, Appli
10	442.5	65.1	236	10	US-09-859-053-30	Sequence 30, Appli
11	441	64.9	241	11	US-09-221-945-1	Sequence 1, Appl
12	437.5	64.3	131	8	US-08-779-788-21	Sequence 21, Appl
13	435.5	64.0	234	9	US-09-740-002-24	Sequence 24, Appl
14	434.5	63.9	128	9	US-09-764-304-10	Sequence 10, Appl
15	434.5	63.9	128	9	US-09-764-304-19	Sequence 19, Appl
16	434.5	63.9	128	12	US-10-166-626-10	Sequence 10, Appl
17	434.5	63.9	128	12	US-10-166-626-19	Sequence 19, Appl
18	434.5	63.9	128	15	US-10-265-713-10	Sequence 10, Appl
19	434.5	63.9	128	15	US-10-265-713-19	Sequence 19, Appl
20	431.5	63.5	108	9	US-09-229-200A-11	Sequence 11, Appl
21	431.5	63.5	108	9	US-09-229-200A-15	Sequence 15, Appl
22	431.5	63.5	108	9	US-09-229-200A-16	Sequence 16, Appl
23	429.5	63.2	127	15	US-10-283-349-71	Sequence 71, Appl
24	424.5	62.4	127	15	US-10-084-139-2	Sequence 2, Appli
25	424.5	62.4	259	12	US-10-053-530-13	Sequence 13, Appl
26	424.5	62.4	259	15	US-10-207-655-13	Sequence 13, Appl
27	420.5	61.8	234	9	US-09-800-729-150	Sequence 150, App
28	418.5	61.5	142	9	US-09-797-481-2	Sequence 2, Appli
29	418.5	61.5	142	9	US-09-844-736-4	Sequence 4, Appli
30	418.5	61.5	142	15	US-10-162-396-4	Sequence 4, Appli
31	417.5	61.4	127	11	US-09-977-283A-7	Sequence 7, Appli
32	416.5	61.3	127	15	US-10-283-349-88	Sequence 88, Appl
33	416	61.2	234	9	US-09-740-002-26	Sequence 26, Appl
34	414.5	61.0	128	9	US-09-855-271-26	Sequence 26, Appl
35	413.5	60.8	125	10	US-09-809-739-1	Sequence 1, Appli
36	413.5	60.8	127	15	US-10-084-139-6	Sequence 6, Appli
37	413	60.7	237	9	US-09-056-160B-100	Sequence 100, App
38	413	60.7	491	14	US-10-011-125-2	Sequence 2, Appli
39	412.5	60.7	127	12	US-10-289-181-8	Sequence 8, Appli
40	411.5	60.5	108	9	US-09-905-243-73	Sequence 73, Appl
41	410.5	60.4	107	12	US-10-330-613-26	Sequence 26, Appl
42	410.5	60.4	107	12	US-10-330-530-26	Sequence 26, Appl
43	410.5	60.4	127	11	US-09-977-283A-17	Sequence 17, Appl
44	409.5	60.2	127	15	US-10-283-349-92	Sequence 92, Appl
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ALIGNMENTS

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RESULT 1
US-10-335-394-16
;  Sequence 16, Application US/10335394
;  Publication No. US2003013845A1
;  GENERAL INFORMATION:
;    APPLICANT: Kwak, Larry
;    APPLICANT: Biragyn, Arya
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS OF
;    TITLE OF INVENTION:  CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
;    FILE REFERENCE: 14014.0316/P
;    CURRENT APPLICATION NUMBER: US/10/335,394
;    CURRENT FILING DATE:  2002-12-31
;    PRIOR APPLICATION DATE: 2000-09-12
;    PRIOR APPLICATION NUMBER: US/09/646,028
;    PRIOR APPLICATION NUMBER: 60/077,745
;    PRIOR FILING DATE: 1998-03-12
;    NUMBER OF SEQ ID NOS: 57
;    SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 16
;    LENGTH: 359
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-16

  Query Match             79.3%;  Score 539;  DB 12;  Length 359;
  Best Local Similarity   91.8%;  Pred. No. 6.2e-42;
  Matches 101;  Conservative  4; Mismatches  5;  Indels  0;  Gaps  0;

Qy    17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
          |:||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db   229 GGSGDIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQP 288

Qy    77 GIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   289 GIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 338
```

```
Qy    81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
          ||||||||||||::|||||||||||||||||||||:||||||||||
Db   155 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 200
```

RESULT 4
US-09-229-200A-7
; Sequence 7, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
;   APPLICANT: Jolliffe et al.
;   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Johnson & Johnson
;   STREET: One Johnson & Johnson Plaza
;   CITY: New Brunswick
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08933-7003
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;   COMPUTER: IBM
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: <Unknown>
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/229,200A
;   FILING DATE: 13-Jan-1999
;   CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: John W. Wallen, III
;   REGISTRATION NUMBER: 35,403
;   REFERENCE/DOCKET NUMBER: ORT-948
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (858) 784-3239
;   TELEFAX: (908) 524-2808
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 109
;   TYPE: amino acid
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-229-200A-7

Query Match   72.1%; Score 490; DB 9; Length 109;
Best Local Similarity 86.1%; Pred. No. 5.6e-38;
Matches 93; Conservative 8; Mismatches 5; Indels 2; Gaps 1;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
          |||||||||||||||||||||| ||:||||||| ::||||||| ||||||:||||||||
Db   1 DIQMTQSPSSLSASLGGKVTIACKASQDINNYIAWYQHKPGKGPRLLIYHTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
          ||||||||||||::|||||||||||||||||||::|::|:|||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCIQYNDLFLTFGGGTKLEIK 108
```

RESULT 5
US-09-229-200A-17
; Sequence 17, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
;   APPLICANT: Jolliffe et al.
;   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Johnson & Johnson
;   STREET: One Johnson & Johnson Plaza
;   CITY: New Brunswick
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08933-7003

RESULT 2
US-10-335-394-13
; Sequence 13, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
;   APPLICANT: Kwak, Larry
;   APPLICANT: Biragyn, Arya
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
;   TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
;   FILE REFERENCE: 14014.0316/P
;   CURRENT APPLICATION NUMBER: US/10/335,394
;   CURRENT FILING DATE: 2002-12-31
;   PRIOR APPLICATION NUMBER: US/09/646,028
;   PRIOR FILING DATE: 2000-09-12
;   PRIOR APPLICATION NUMBER: 60/077,745
;   PRIOR FILING DATE: 1998-03-12
;   NUMBER OF SEQ ID NOS: 57
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-13

Query Match   79.3%; Score 539; DB 12; Length 361;
Best Local Similarity 91.8%; Pred. No. 6.2e-42;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy   17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
          |: |||||||||||||||||||||| |||||||| :||||||||||||| ||||||||
Db   231 GSGSDIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQP 290

Qy   77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
          |||||||||||||::||||||||||||||||||||||:|||||||||
Db   291 GIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 340
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RESULT 3
US-10-335-394-15
; Sequence 15, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
;   APPLICANT: Kwak, Larry
;   APPLICANT: Biragyn, Arya
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
;   TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
;   FILE REFERENCE: 14014.0316/P
;   CURRENT APPLICATION NUMBER: US/10/335,394
;   CURRENT FILING DATE: 2002-12-31
;   PRIOR APPLICATION NUMBER: US/09/646,028
;   PRIOR FILING DATE: 2000-09-12
;   PRIOR APPLICATION NUMBER: 60/077,745
;   PRIOR FILING DATE: 1998-03-12
;   NUMBER OF SEQ ID NOS: 57
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
;   LENGTH: 374
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-15

Query Match          78.7%;  Score 535;  DB 12;  Length 374;
Best Local Similarity 94.3%;  Pred. No. 1.5e-41;
Matches 100;  Conservative  3;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
          ||||||||||||||||||||||||| |||||||| ||||||||||| |||||||| ||||||
Db    95 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 154
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```
                        GenCore version 5.1.6
            Copyright (c) 1993 - 2003 Compugen Ltd.

QM protein - protein search, using sw model

Run on:      October 7, 2003, 09:09:40 ; Search time 17.8182 Seconds
                                          (without alignments)
                                          680.050 Million cell updates/sec

Title:    US-09-155-739-2
Perfect score: 680
Sequence:  1 MRPSIQFLGLLLFWLHGAQC.........YCLQYDNLWTFGGGTKLEIK 126
Scoring table: BLOSUM62
           Gapop 10.0 , Gapext 0.5

Searched:  283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:        283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_76:*
             1: piri:*
             2: pir2:*
             3: pir3:*
             4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES
```

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	589	86.6	125	2	S09365	Ig kappa chain - m
2	535	78.7	104	2	S26330	Ig kappa chain v r
3	526	77.4	104	2	S26329	Ig kappa chain v r
4	524	77.1	106	2	C33936	Ig kappa chain v r
5	490.5	72.1	129	2	S52789	Ig kappa chain v r
6	490	72.1	103	2	S26332	Ig light chain v r
7	488	71.8	97	2	PH1064	Ig light chain v r
8	476	70.0	94	2	E33730	Ig kappa chain v r
9	471.5	69.3	107	2	PL0270	Ig kappa chain v r
10	465.5	68.5	107	2	PL0272	Ig kappa chain v r
11	464.5	68.3	107	2	PL0269	Ig kappa chain v r
12	464.5	68.3	107	2	PL0271	Ig kappa chain v-J
13	453.5	66.7	127	2	S40367	Ig kappa chain - h
14	445.5	65.5	132	2	S40334	Ig kappa chain - h
15	444.5	65.4	139	2	S40365	Ig kappa chain v-J
16	443.5	65.2	129	2	S40317	Ig kappa chain v-J
17	442.5	65.1	125	2	S40333	Ig kappa chain v-J
18	442.5	65.1	131	2	S40352	Ig kappa chain v-J
19	441.5	64.9	129	1	K1HUWK	Ig kappa chain pre
20	439.5	64.6	94	2	PH1063	Ig light chain v r
21	439	64.6	124	2	S40336	Ig kappa chain v-J
22	438.5	64.5	123	2	S40331	Ig kappa chain - h
23	438	64.4	117	2	S42263	Ig kappa chain v r
24	437.5	64.3	122	2	A29380	Ig kappa chain pre
25	437.5	64.3	127	2	S52447	Ig kappa chain pre
26	437.5	64.3	135	2	S24320	Ig kappa chain v r
27	436.5	64.2	128	2	PL0101	Ig kappa chain pre
28	436.5	64.2	129	2	S52793	Ig kappa chain v r
29	435.5	64.0	127	2	S04574	Ig kappa chain pre
30	435.5	64.0	127	2	S11240	Ig kappa chain v r
31	434.5	63.9	141	2	A49134	Ig kappa chain V-I
32	433.5	63.7	126	2	A34904	Ig kappa chain pre
33	433.5	63.7	234	2	S14237	Ig kappa chain v r
34	432	63.5	117	2	S43528	Ig kappa chain V r
35	430.5	63.3	127	2	PH1224	Ig kappa chain pre
36	428.5	63.0	125	2	S40316	Ig kappa chain - h
37	427.5	62.9	129	2	S52792	Ig kappa chain v r
38	426.5	62.7	125	2	S40350	Ig kappa chain - h
39	425.5	62.6	125	2	S40349	Ig kappa chain V-J
40	425.5	62.6	128	1	KVMST1	Ig kappa chain pre
41	422.5	62.1	124	2	S40348	Ig kappa chain V-J
42	419.5	61.7	122	2	S40314	Ig kappa chain - h
43	419.5	61.7	124	2	S03521	Ig kappa chain pre
44	418	61.5	127	2	A23986	Ig kappa chain V r
45	416.5	61.3	85	2	F36025	Ig light chain V r

```
                        ALIGNMENTS

RESULT 1
S09365
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09365
R;Feddersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene
A;Reference number: S09365; MUID:90098844; PMID:2513557
A;Accession: S09365
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match    86.6%;  Score 589;  DB 2;  Length 125;
Best Local Similarity  90.6%;  Pred. No. 6.1e-44;
Matches 115;  Conservative  2;  Mismatches  2;  Indels  4;  Gaps  2;

Qy      1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
            ||||||||||||||||||||    ||||||||||||||||||||| ||||||| |||||
Db      1 MRPSIQFLGLLLFWLHG---DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKP 57

Qy     61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW-TFGG 119
           ||||||||||| |||||||||||||| |||:|||||||| |||||||||||||| ||||
Db     58 GKGPRLLIHYSTLQPGIPSRFSGSGSGDYSFSISNLGPEDIATYYCLQYDNLLRTFGG 117

Qy    120 GTKLEIK 126
           |||||||
Db    118 GTKLEIK 124

RESULT 2
S26330
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26330
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a prote
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26330
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59185; NID:g52316; PIDN:CAA41895.1; PID:g1334063
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
```

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   78.7%;   Score 535; DB 2; Length 104;
Best Local Similarity   95.2%;   Pred. No. 2.3e-39;
Matches   99; Conservative   2; Mismatches   3; Indels   0; Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
            ||||||||||||||||||||| |||||||||||:||||||||||| |||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLE 124
            |||||||||||||||||||||||||:||||||||||||||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLE 104

RESULT 3
S26329
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   77.4%;   Score 526; DB 2; Length 104;
Best Local Similarity   94.2%;   Pred. No. 1.3e-38;
Matches   98; Conservative   3; Mismatches   3; Indels   0; Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
            ||||||||||||||||||||||||| ||||||||:||||||||| ||||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLE 124
            |||||||||||||||||||||||||:||||||||||||||||||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLE 104

RESULT 4
C33936
Ig kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831; PMID:2471975
A;Accession: C33936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   77.1%;   Score 524; DB 2; Length 106;
Best Local Similarity   91.5%;   Pred. No. 2e-38;
Matches   97; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
            |||||||||||||||||||||||||||||||||||||||||| |||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYLAWTYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
            |||||||||||||||||:|||:||||||||||:||||||||||||
Db   61 RFSGSGSGRDYSFSISNLDPEIATYYCLQYDSLYTFGGGTKLEIK 106

RESULT 5
S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; De
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myel
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match   72.1%;   Score 490.5; DB 2; Length 129;
Best Local Similarity   72.4%;   Pred. No. 1.9e-35;
Matches   92; Conservative   15; Mismatches   19; Indels   1; Gaps   1;

Qy   1 MRPSIQFLGLLLFWLWGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
            || ||||| | ||||||||:|||||||||||||||||: |||||: ||| ||
Db   3 MRVPAQLLGLLLWLSGARCDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKP 62

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
            || |:|||| |:||||||||||||||||||||:||| || | |:|||||||:||| |:||
Db   63 GKAPKLLIHAASSLETGVPSRFSGSGSGTDFSFTISSLQPEDIATYYCQQYDNLPLTFGG 122

Qy   120 GTKLEIK 126
            ||:|||
Db   123 GTKVEIK 129

RESULT 6
S26332
Ig light chain V region - mouse (fragment)
N;Alternate names: Ig kappa chain V region
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332; S26331
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26332
A;Molecule type: mRNA
A;Residues: 1-103 <STA>
A;Cross-references: EMBL:X59187; NID:g52318; PIDN:CAA41897.1; PID:g1334064
A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are
A;Accession: S26331
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <ST2>
A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   72.1%;   Score 490; DB 2; Length 103;
Best Local Similarity   87.4%;   Pred. No. 1.7e-35;
Matches   90; Conservative   7; Mismatches   6; Indels   0; Gaps   0;

Qy   21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
            |||||||||||||||||||||| ||| ||:||||||||||||| ||||||||
Db   1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYLAWYQHKPGKGPRLLIHYTSTLQPGIPS 80

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                GenCore version 5.1.6
        Copyright (C) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:     October  7, 2003, 09:02:30 ; Search time 9.41818 Seconds
                                         (without alignments)
                                         629.141 Million cell updates/sec

Title:          US-09-155-739-2
Perfect score:  680
Sequence:       1 MRPSIQFLGLLLFWLHGAQC.........YCLQYDNLWTFGGGTKLEIK 126

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:       127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SwissProt_41:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                        SUMMARIES
```

Result No.	Score	Query Match %	Length	DB	ID	Description
1	441.5	64.9	129	1	KV1W_HUMAN	P04431 homo sapien
2	425.5	62.6	128	1	KV5E_MOUSE	P01637 mus musculu
3	412.5	60.7	129	1	KV1X_HUMAN	P04432 homo sapien
4	402	59.1	117	1	KV1J_HUMAN	P01602 homo sapien
5	400	58.8	115	1	KV5F_MOUSE	P01638 mus musculu
6	397.5	58.5	108	1	KV1B_HUMAN	P01594 homo sapien
7	395.5	58.2	108	1	KV1O_HUMAN	P01607 homo sapien
8	392.5	57.7	108	1	KV1P_HUMAN	P01608 homo sapien
9	389.5	57.3	108	1	KV1Y_HUMAN	P80362 homo sapien
10	380.5	56.0	108	1	KV1A_HUMAN	P01593 homo sapien
11	379.5	55.8	108	1	KV1M_HUMAN	P01605 homo sapien
12	378.5	55.7	130	1	KV5G_MOUSE	P01639 mus musculu
13	378.5	55.7	133	1	KV4B_HUMAN	P06313 homo sapien
14	378	55.6	117	1	KV1I_HUMAN	P01601 homo sapien
15	377.5	55.5	108	1	KV5J_MOUSE	P01643 mus musculu
16	377	55.4	107	1	KV1D_HUMAN	P01596 homo sapien
17	375	55.1	134	1	KV4C_HUMAN	P06314 homo sapien
18	374.5	55.1	108	1	KV5O_MOUSE	P01648 mus musculu
19	373.5	54.9	108	1	KV1Q_HUMAN	P01609 homo sapien
20	373.5	54.9	108	1	KV5N_MOUSE	P01647 mus musculu
21	371.5	54.6	108	1	KV5K_MOUSE	P01644 mus musculu
22	369.5	54.3	108	1	KV5M_MOUSE	P01646 mus musculu
23	368.5	54.2	108	1	KV5L_MOUSE	P01645 mus musculu
24	366.5	53.9	108	1	KV1R_HUMAN	P01610 homo sapien
25	362.5	53.3	108	1	KV1C_HUMAN	P01595 homo sapien
26	360.5	53.0	108	1	KV1H_HUMAN	P01600 homo sapien
27	359.5	52.9	108	1	KV1N_HUMAN	P01606 homo sapien
28	357.5	52.6	108	1	KV1E_HUMAN	P01597 homo sapien
29	357.5	52.6	108	1	KV1V_HUMAN	P04430 homo sapien
30	355.5	52.3	108	1	KV1F_HUMAN	P01598 homo sapien
31	354.5	52.1	108	1	KV1S_HUMAN	P01611 homo sapien
32	353.5	52.0	115	1	KV5C_MOUSE	P01635 mus musculu
33	352.5	51.8	108	1	KV1K_HUMAN	P01603 homo sapien
34	350.5	51.5	108	1	KV1L_HUMAN	P01604 homo sapien
35	349.5	51.4	108	1	KV5U_MOUSE	P04946 mus musculu
36	347	51.0	129	1	KV3H_HUMAN	P04207 homo sapien
37	347	51.0	129	1	KV3M_HUMAN	P18136 homo sapien
38	343	50.4	117	1	KV5H_MOUSE	P01641 mus musculu
39	341.5	50.2	108	1	KV1G_HUMAN	P01599 homo sapien
40	341	50.1	110	1	KV3P_MOUSE	P01668 mus musculu
41	339.5	49.9	108	1	KV5T_MOUSE	P01653 mus musculu
42	338	49.7	129	1	KV3L_HUMAN	P18135 homo sapien
43	337.5	49.6	131	1	KV3I_MOUSE	P01661 mus musculu
44	335.5	49.3	108	1	KV5P_MOUSE	P01649 mus musculu
45	335.5	49.3	108	1	KV5Q_MOUSE	P01650 mus musculu

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                        ALIGNMENTS

RESULT 1
KV1W_HUMAN
ID   KV1W_HUMAN      STANDARD;      PRT;     129 AA.
AC   P04431;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Walker precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use by non-profit institutions as long as its content is in no  way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X00965; CAA25477.1; ALT_TERM.
DR   PIR; A01883; KIHUWK.
DR   HSSP; P01607; 1REI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION WALKER.
FT   DOMAIN       23     45       FRAMEWORK-1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      120    129       FRAMEWORK-4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;

     Query Match             64.9%;  Score 441.5;  DB 1;  Length 129;
     Best Local Similarity   66.9%;  Pred. No. 1.7e-38;
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Matches 85; Conservative 15; Mismatches 26; Indels 1; Gaps 1;

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Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         || : |||||| ||      :||||||||||||||||||| :||||:::| ::||||
Db    3 MRVPAQLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKP 62

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
         || |:|||          ||||||||||| |:: |||||:|| | |:  | | |||
Db   63 GKAPKLLIYAASSLQSGVTSRFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLITFGQ 122

Qy  120 GTKLEIK 126
         ||:|||
Db  123 GTRLEIK 129
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RESULT 2
KV5E_MOUSE
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ID   KV5E_MOUSE    STANDARD;    PRT;    128 AA.
AC   P01637;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-v region T1 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81052342; PubMed=6776411;
RA   Altenburger W., Steinmetz M., Zachau H.G.;
RT   "Functional and non-functional joining in immunoglobulin light chain
RT   genes of a mouse myeloma.";
RL   Nature 287:603-607(1980).
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DR   EMBL; V00772; CAA24150.1; -.
DR   PIR; A01920; KVMST1.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    128       IG KAPPA CHAIN V-V REGION T1.
FT   DOMAIN       21     43       FRAMEWORK-1.
FT   DOMAIN       44     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     69       FRAMEWORK-2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       77    108       FRAMEWORK-3.
FT   DOMAIN      109    117       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      118    127       FRAMEWORK-4.
FT   DISULFID     43    108       BY SIMILARITY.
FT   NON_TER     128    128
SQ   SEQUENCE  128 AA;  14385 MW;  AFA5563D31BB7E05 CRC64;
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Query Match   62.68%; Score 425.5; DB 1; Length 128;
Best Local Similarity 62.2%; Pred. No. 7.5e-37;
Matches 79; Conservative 18; Mismatches 29; Indels 1; Gaps 1;

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Qy    1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
         || : |||||| ||      :|||||||||||||||| : |||: :|: ||||
Db    1 MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTISCKASQDINSYLTWFQQKP 60
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Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
         || |:|:  : .| :.||||||||||||:::| ||: |||||| |||
Db   61 GKSPKTLLYRANRLVDGVPSRFSGSGSGQDFSLTISSLRYEDMGIYYCLQYDEFPLTFGA 120

Qy  120 GTKLEIK 126
         |||:||
Db  121 GTKLELK 127
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RESULT 3
KV1X_HUMAN
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ID   KV1X_HUMAN    STANDARD;    PRT;    129 AA.
AC   P04432;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Daudi precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
```

```
DR   EMBL; X00966; CAA25478.1; ALT_TERM.
DR   PIR; A01884; K1HUDI.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION DAUDI.
FT   DOMAIN       23     45       FRAMEWORK-1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      120    129       FRAMEWORK-4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE  129 AA;  14235 MW;  CAF076BC7E5574C8 CRC64;
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Query Match   60.7%; Score 412.5; DB 1; Length 129;
Best Local Similarity 61.4%; Pred. No. 1.6e-35;
Matches 78; Conservative 19; Mismatches 29; Indels 1; Gaps 1;

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         || : |||||| ||      :|||||||||||||||||||: :|||||:  :| ::||||
Db    3 MRVPAQLGLLLLWLRRVRCDIQMTQSPSSLSASVGDRVTITCRAGHNINFLSWYQQKP 62

Qy   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:        October 7, 2003, 09:01:50 ; Search time 61.0909 Seconds
                                     (without alignments)
                                     363.748 Million cell updates/sec

Title:          US-09-155-739-4
Perfect score:  746
Sequence:       1 MKCSWVMFFLMAVVTGVNSE........YGNYGVYAMDYWGQGTSVTV 140

Scoring table:  BLOSUM62
                GapOp 10.0 , GapExt 0.5

Searched:       1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:     1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      A_Geneseq_19Jun03:*
          1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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         24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	746	100.0	140	16	AAR81327	Mouse VLA-4 antibo
2	746	100.0	140	18	AAW22410	Alpha-4 integrin m
3	645	86.5	123	16	AAR81330	Mouse anti-VLA-4 a
4	633	84.9	136	17	AAW04379	Chimaeric human/mu
5	629	84.3	140	12	AAR11384	Variable gamma hea
6	625	83.8	136	16	AAR76664	Murine ONS-21 anti
7	595	79.8	136	14	AAR41679	V heavy chain of r
8	593.5	79.6	137	18	AAW21845	Heavy chain variab
9	591	79.2	138	19	AAW63828	Human Mab #117-10C
10	584	78.3	142	16	AAR81333	Human VLA-4 reshap
11	584	78.3	142	18	AAW22428	Humanised alpha-4
12	576.5	77.3	135	21	AAB07967	Amino acid sequenc
13	570.5	76.5	137	17	AAR95948	HNR-20 variable he
14	544	72.9	123	16	AAR81323	Humanized VLA-4 an
15	539.5	72.3	135	21	AAB07969	A heavy chain vari
16	537	72.0	123	18	AAW22413	Humanised alpha-4
17	535.5	71.8	437	19	AAW37738	Nucleotide sequenc
18	527	70.6	119	24	ABP97650	Amino acid sequenc
19	524.5	70.3	122	21	AAY53590	Heavy chain from a
20	521.5	69.9	120	14	AAR30767	Heavy chain variab
21	521.5	69.9	120	14	AAW44121	Heavy chain variab
22	521.5	69.9	120	23	AAU79031	Mouse antibody NR-
23	518.5	69.5	113	15	AAR60527	Heavy chain variab
24	517	69.3	143	15	AAR59942	Anti-VLA4 rAb huma
25	516.5	69.2	120	16	AAR79889	Anti-EGFR antibody
26	516.5	69.2	150	24	AAE33371	Hybridoma 902 immu
27	516	69.2	121	20	AAW96741	Heavy chain variab
28	516	69.2	121	24	ABU08538	Mouse anti-VLA-4 a
29	513	68.8	121	24	AAW96744	Heavy chain variab
30	513	68.8	121	20	ABU08543	Mouse anti-VLA-4 a
31	513	68.8	138	22	AAG66455	VEGF ScFv protein
32	511	68.5	120	14	AAR39817	HP1/2 Vh. Homo sa
33	511	68.5	120	15	AAR58749	Anti-VLA4 Ab HP1/2
34	511	68.5	120	20	AAY23984	Antibody HP1/2 hea
35	511	68.5	120	20	AAY01033	Anti VLA-4 antibod
36	511	68.5	120	22	AAB73462	Murine anti-VLA-4
37	509.5	68.3	126	12	AAR15439	Heavy chain variab
38	508	68.1	120	14	AAR39566	Sequence of the va
39	507.5	68.0	133	23	ABB75617	Anti-RANK ligand m
40	505.5	67.8	138	21	AAY56873	MAb CT-M-01 heavy
41	505.5	67.8	139	18	AAW29750	Anti-HMFG MAb CTMO
42	504	67.6	254	20	AAY30117	Murine anti-botuli
43	504	67.6	254	20	AAY30119	Murine anti-botuli
44	504	67.6	254	20	AAY30121	Murine anti-botuli
45	504	67.6	254	20	AAY30123	Murine anti-botuli

ALIGNMENTS

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RESULT 1
AAR81327
ID   AAR81327 standard; Protein; 140 AA.
XX
AC   AAR81327;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light heavy variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Region          20..49
FT                   /note= "framework region 1"
FT   Region          50..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..68
FT                   /note= "framework region 2"
FT   Region          69..85
FT                   /note= "complementarity determining region 2"
FT   Region          86..117
FT                   /note= "framework region 3"
FT   Region          118..131
FT                   /note= "complementarity determining region 3"
FT   Region          132..140
FT                   /note= "framework region 4"
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XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995; 95WO-US01219.
XX
PR   25-JAN-1994; 94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99892.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 2; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 heavy chain variable
CC   region directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized heavy chain, amino acids H27,
CC   H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig H chain. Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells. The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis. They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis. The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence 140 AA;

Query Match   100.0%; Score 746; DB 16; Length 140;
Best Local Similarity   100.0%; Pred. No. 1e-59;
Matches 140; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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Db   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120

Qy   121 YGNYGVYAMDYWGQGTSVTV 140
              ||||||||||||||||||||
Db   121 YGNYGVYAMDYWGQGTSVTV 140

RESULT 2
AAW22410
ID   AAW22410 standard; Protein; 140 AA.
XX
AC   AAW22410;
XX
DT   08-DEC-1997 (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VH region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
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PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996; 96WO-US18807.
XX
PR   21-NOV-1995; 95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74760.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 18; Page 69-70; 107pp; English.
XX
CC   This polypeptide comprises the heavy chain variable region (VH) of
CC   mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC   complementarity determining regions (CDRs) of the 21.6 VH can be
CC   incorporated into a human 21/28'CL framework to produce a claimed
CC   humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6
CC   antibody that is used in the manufacture of a medicament for
CC   treating a disease selected from asthma, atherosclerosis, AIDS,
CC   dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   metastasis, nephritis, graft versus host disease, tumour
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibodies of the
CC   invention have a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
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SQ   Sequence 140 AA;

Query Match   100.0%; Score 746; DB 18; Length 140;
Best Local Similarity   100.0%; Pred. No. 1e-59;
Matches 140; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

OM protein - protein search, using sw model

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          GenCore version 5.1.6
    Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: October 7, 2003, 09:10:55 ; Search time 18.101 Seconds
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Perfect score: 746
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Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	746	100.0	140	5	PCT-US95-01219-4	Sequence 4, Appl1
3	645	86.5	123	5	US-08-561-521-9	Sequence 9, Appl1
4	645	86.5	123	5	PCT-US95-01219-9	Sequence 9, Appl1
5	633	84.9	136	1	US-08-646-253A-29	Sequence 29, Appl1
6	595	79.8	136	3	US-08-024-253-2	Sequence 2, Appl1
7	593.5	79.6	137	3	US-08-836-561-31	Sequence 31, Appl1
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10	584	78.3	142	5	PCT-US95-01219-17	Sequence 17, Appl1
11	562	75.3	125	2	US-08-561-521-44	Sequence 44, Appl1
12	562	75.3	125	5	PCT-US95-01219-44	Sequence 44, Appl1
13	554	74.3	136	3	US-08-348-548-8	Sequence 8, Appl1
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16	544	72.9	123	5	PCT-US95-01219-11	Sequence 11, Appl1
17	528.5	70.8	120	5	US-07-934-373C-6	Sequence 6, Appl1
18	528.5	70.8	120	3	US-08-437-642B-6	Sequence 6, Appl1
19	528.5	70.8	120	4	US-08-146-206C-6	Sequence 6, Appl1
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21	521.5	69.9	120	5	US-08-871-488A-15	Sequence 15, Appl1
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23	516	69.2	121	4	US-09-157-452B-2	Sequence 13, Appl1
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35	504	67.6	254	3	US-08-792-824-13	Sequence 13, Appl1
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ALIGNMENTS

RESULT 1
US-08-561-521-4
; Sequence 4, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/561,521
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/186,269A
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 140 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-4

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; Sequence 4, Application PCT/US9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
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;   FILING DATE: 25-JAN-1995
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
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;   TYPE: amino acid
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; Sequence 9, Application US/08561521
; Patent No. 584029
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
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;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/561,521
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/186,269A
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 123 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-9

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Qy 140 V 140
Db 121 V 121

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; Sequence 9, Application PCT/TUS9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose

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                GenCore version 5.1.6
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Title:         US-09-155-739-4
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Total number of hits satisfying chosen parameters:      587654

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	521.5	69.9	120	15	US-10-056-794-15	Sequence 15, Appl
4	516	69.2	121	15	US-10-252-978-2	Sequence 2, Appl
5	513	68.8	121	15	US-10-252-978-16	Sequence 16, Appl
6	511	68.5	120	15	US-10-095-496-1	Sequence 1, Appll
7	502	67.3	136	11	US-09-749-873-99	Sequence 99, Appl
8	495.5	66.4	116	11	US-09-910-483-37	Sequence 37, Appl
9	495.5	66.4	116	11	US-09-910-483-41	Sequence 41, Appl
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15	488.5	65.5	136	10	US-09-963-620-11	Sequence 11, Appl
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18	488.5	65.5	136	11	US-10-225-779-11	Sequence 11, Appl
19	488.5	65.5	136	15	US-10-225-784-11	Sequence 11, Appl
20	483.5	64.8	139	10	US-09-809-739-5	Sequence 5, Appll
21	475.5	63.7	535	10	US-09-968-851-38	Sequence 38, Appl
22	475	63.7	117	10	US-09-158-120A-18	Sequence 18, Appl
23	473.5	63.5	153	9	US-09-861-294-4	Sequence 4, Appll
24	473.5	63.5	153	12	US-10-367-506-4	Sequence 4, Appl
25	467.5	62.7	112	14	US-10-032-482-7	Sequence 7, Appl
26	466.5	62.5	120	10	US-09-910-059-11	Sequence 11, Appl
27	463	62.1	117	11	US-09-802-083-1	Sequence 1, Appl
28	463	62.1	117	12	US-10-172-785-1	Sequence 1, Appl
29	463	62.1	117	15	US-10-165-732A-1	Sequence 1, Appl
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31	461	61.8	117	10	US-09-865-198-22	Sequence 22, Appll
32	461	61.8	117	11	US-09-798-689-7	Sequence 7, Appll
33	461	61.8	238	9	US-09-976-787-29	Sequence 29, Appl
34	461	61.8	238	10	US-09-865-198-28	Sequence 28, Appl
35	461	61.8	238	11	US-09-798-689-21	Sequence 21, Appl
36	460	61.7	117	9	US-09-976-787-7	Sequence 7, Appll
37	460	61.7	117	10	US-09-865-198-7	Sequence 28, Appl
38	460	61.7	240	9	US-09-976-787-28	Sequence 27, Appl
39	460	61.7	240	10	US-09-865-198-27	Sequence 78, Appl
40	457	61.3	138	9	US-09-753-436-78	Sequence 7, Appll
41	456	61.1	468	11	US-09-795-515-7	Sequence 7, Appll
42	455	61.0	140	9	US-09-748-960-4	Sequence 4, Appll
43	455	61.0	140	15	US-10-283-349-27	Sequence 27, Appl
44	455	61.0	269	11	US-09-749-873-109	Sequence 109, App
45	454.5	60.9	135	12	US-10-244-821-91	Sequence 91, Appl

ALIGNMENTS

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RESULT 1
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; Sequence 29, Application US/09749873
; Publication No. US2003002304SA1
; GENERAL INFORMATION:
;   APPLICANT: OHTOMO, Toshihiko
;              SATO, Koh
;              TSUCHIYA, Masayuki
;   TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                       MEDULLOBLASTOMA CELLS
;   NUMBER OF SEQUENCES: 132
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: 3000 K Street, N.W., Suite 500
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20007-5109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/749,873
;     FILING DATE: 29-Dec-2000
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/646,265
;     FILING DATE: 1996-09-09
;     APPLICATION NUMBER: JP 5-291078
;     FILING DATE: 19-NOV-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: WEGNER, Harold C.
;     REGISTRATION NUMBER: 25,258
;     REFERENCE/DOCKET NUMBER: 53466/184
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202)672-5300
```

```
             TELEFAX: (202)672-5399
             TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 136 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;    MOLECULE TYPE: protein
;    SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-749-873-29

Query Match             84.9%;  Score 633;  DB 11;  Length 136;
Best Local Similarity   89.3%;  Pred. No. 3.1e-56;
Matches 125;  Conservative  2;  Mismatches  7;  Indels  6;  Gaps  2;

Qy    1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db    1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHWAKQRP 60

Qy   61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           ||||||||||||  ||||||||||||||||||||||||||||||||||||||:||
Db   61  EQGLEWIGRIDPADGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCA-SAY 119

Qy  121  YGNYGVYAMDYWGQGTSVTV 140
           |   ||||||||||
Db  120  YVN----QDYWGQGTSVTV 134

RESULT 2
US-10-283-349-31
; Sequence 31, Application US/10283349
; Publication No. US20030096977A1
;  GENERAL INFORMATION:
;    APPLICANT: KOIKE, Masamichi
;               FURUYA, Akiko
;               NAKAMURA, Kazuyasu
;               IIDA, Akihiro
;               ANAZAWA, Hideharu
;               HANAI, NO. US20030096977Aluo
;               TAKATSU, Kiyoshi
;    TITLE OF INVENTION: Antibody Against Human Interleukin-5
;               Receptor Alpha Chain
;    NUMBER OF SEQUENCES: 106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Pennie & Edmonds LLP
;      STREET: 1155 Avenue of the Americas
;      CITY: New York
;      STATE: NY
;      COUNTRY: USA
;      ZIP: 10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: DOS
;      SOFTWARE: FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/283,349
;      FILING DATE: 29-Oct-2002
;      CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/08/836,561
;      FILING DATE: 09-MAY-1997
;      APPLICATION NUMBER: JP 232384/95
;      FILING DATE: 11-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Lawrence, III, Stanton T
;      REGISTRATION NUMBER: 25,736
;      REFERENCE/DOCKET NUMBER: 7005-115-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 212-790-9090
;      TELEFAX: 212-869-9741
;      TELEX: 66141 PENNIE
;  INFORMATION FOR SEQ ID NO: 31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 137 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: peptide
;    SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-283-349-31

Query Match             79.6%;  Score 593.5;  DB 15;  Length 137;
Best Local Similarity   82.9%;  Pred. No. 2.9e-52;
Matches 116;  Conservative  6;  Mismatches  13;  Indels  5;  Gaps  1;

Qy    1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||:||||||||||||||||||||||||||||||:||||||||||||:|  ||||
Db    1  MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVKPGASVNLSCTASGFNIKDTYMHWVKQRP 60

Qy   61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           ||||||||||||| |:|  |||||:|||| :||||||||||||||||||||||:|
Db   61  EQGLEWIGRIDPANGNTKSDPKFQAKATTAADTSNTAYLQLSSLTSEDTAVYYCT---- 116

Qy  121  YGNYGVYAMDYWGQGTSVTV 140
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Db  117  -GGLRLRFPDYWGQGTTLTV 135

RESULT 3
US-10-056-794-15
; Sequence 15, Application US/10056794
; Publication No. US20030119078A1
;  GENERAL INFORMATION:
;    APPLICANT: Graves, Scott S.
;               Reno, John M.
;               Mallett, Robert W.
;               Hylarides, Mark D.
;               Searle, Stephen M.J.
;               Henry, Andrew H.
;               Pedersen, Jan T.
;               Rees, Anthony R.
;    TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE
;               ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN
;               PRETARGETING METHODS
;    NUMBER OF SEQUENCES: 19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Seed IP Law Group
;      STREET: 701 Fifth Avenue, Suite 6300
;      CITY: Seattle
;      STATE: Washington
;      COUNTRY: USA
;      ZIP: 98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/056,794
;      FILING DATE: 24-Jan-2002
;      CLASSIFICATION: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Sharkey Ph.D., Richard G.
;      REGISTRATION NUMBER: 32,629
;      REFERENCE/DOCKET NUMBER: 690022.527C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206) 622-4900
;      TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 120 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;    MOLECULE TYPE: protein
;    SEQUENCE DESCRIPTION: SEQ ID NO: 15:
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                GenCore version 5.1.6
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  7, 2003, 09:09:40 ; Search time 19.798 Seconds
                                       (without alignments)
                                       680.050 Million cell updates/sec

Title:          US-09-155-739-4
Perfect score:  746
Sequence:       1 MKKCSWVMFFLMAVVTGVNSE.........YGNYGVYAMDYWGQGTSVTV 140

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:  283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:    283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR_76:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match %	Match Length	DB	ID	Description
1	603.5	80.9	178	2	S29594	Ig gamma chain (WM
2	597	80.0	136	2	S04576	Ig heavy chain pre
3	570.5	76.5	137	2	S52445	Ig heavy chain V r
4	567.5	76.1	123	2	PH1403	Ig heavy chain V r
5	539	72.3	120	2	S03471	Ig heavy chain V-D
6	523	70.1	117	2	S17586	Ig heavy chain V r
7	521.5	69.9	122	2	S06823	Ig heavy chain V r
8	515	69.0	115	2	S03482	Ig heavy chain V-D
9	500	67.0	116	2	S24289	Ig gamma chain V r
10	498	66.8	120	2	S03484	Ig heavy chain V-D
11	494.5	66.3	268	2	A56446	Ig heavy chain V r
12	493.5	66.2	108	2	PH1012	Ig heavy chain V r
13	492	66.0	221	2	S49220	Ig gamma-1 chain -
14	472.5	63.3	114	4	A47271	nitrophenyl phosph
15	471	63.1	107	2	PH1482	Ig heavy chain V r
16	467	62.6	107	2	PH1013	Ig heavy chain pre
17	466.5	62.5	139	2	PS0024	Ig heavy chain pre
18	464.5	62.3	139	1	MHMS18	Ig heavy chain V r
19	462.5	62.0	99	2	D37262	Ig heavy chain V r
20	461.5	61.9	115	2	PL0246	Ig heavy chain V r
21	461.5	61.9	139	2	A27609	Ig heavy chain pre
22	460.5	61.7	141	2	JL0076	Ig heavy chain pre
23	459	61.5	135	2	PH1492	Ig heavy chain V r
24	459	61.5	140	1	HVMSG7	Ig heavy chain pre
25	457.5	61.3	107	2	A27646	Ig heavy chain V r
26	457	61.3	138	2	E32513	Ig heavy chain pre
27	456	61.1	249	2	S41374	single Chain Fv an
28	455.5	61.1	141	2	A39276	Ig heavy chain pre
29	455	61.0	140	2	PH1498	Ig heavy chain V r
30	454.5	60.9	133	2	PC1155	Ig heavy chain pre
31	454	60.9	118	2	S25174	Ig heavy chain V r
32	454	60.9	138	2	S21810	Ig heavy chain V r
33	453	60.7	140	2	PH1484	Ig heavy chain V r
34	452	60.6	135	2	PH1493	Ig heavy chain V r
35	451.5	60.5	469	2	S37483	Ig gamma-2a chain
36	451	60.5	135	2	PH1494	Ig heavy chain V r
37	447	59.9	140	2	PH1489	Ig heavy chain V r
38	444	59.5	140	2	PH1486	Ig heavy chain V r
39	441	59.1	140	2	PH1488	Ig heavy chain V r
40	440.5	59.0	120	2	S41394	Ig heavy chain V r
41	440	59.0	122	2	S20643	Ig heavy chain - m
42	440	59.0	246	2	S38950	Ig gamma chain - m
43	440	59.0	446	2	S40295	Ig gamma-2a chain
44	439	58.8	123	2	S20646	Ig heavy chain V r
45	438	58.7	99	2	C37262	Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
S29594
Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
R;Seymour, R.
submitted to the EMBL Data Library, February 1991
A;Reference number: S29594
A;Accession: S29594
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <SEY>
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin

Query Match   80.9%;   Score 603.5;  DB 2;  Length 178;
Best Local similarity   88.1%;   Pred. No. 1.9e-45;
Matches 118;  Conservative  6;  Mismatches  5;  Indels  5;  Gaps  2;

Qy    7 MFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEW 66
         :||||||||||||||||||||||||||||||||||||||||||:| |||| :|||||
Db    1 IFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEW 60

Qy   67 IGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVFCAREGYYGNYGV 126
         |||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   61 IGRIDPANGYTEYDPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG---GNY-A 115

Qy  127 YAMDYWGQGTSVTV 140
         | |||||||||||
Db  116 YGMDYWGQGTSVTV 129

RESULT 2
S04576
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C;Accession: S04576
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J ,
Eur. J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: invol\
A;Reference number: S04573; MUID:87133856; PMID:3102255
A;Accession: S04576
A;Molecule type: mRNA
A;Residues: 1-136 <KOF>
A;Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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C;Keywords: heterotetramer; immunoglobulin
F;35-118/Domain: immunoglobulin homology <IMM>

Query Match   76.1%;   Score 567.5;   DB 2;   Length 123;
Best Local Similarity   94.9%;   Pred. No. 1.8e-42;
Matches 111;   Conservative   3;   Mismatches 2;   Indels 2;   Gaps 1;

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Qy    1  MKCSWVMFFLMAVVT-GVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQR 59
            |||||:::||||||| ||||||||||||||||||||||||||||||||||||||:| ||||
Db    1  MKCSWVIFFLMAVVTAGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQR 60

Qy   60  PEQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCA 116
            ||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   61  PEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCA 117
```

RESULT 5
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03471
A;Molecule type: mRNA
A;Residues: 7-120 <ROC1>
A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Molnier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A;Reference number: S07453; MUID:83058021; PMID:6815271
A;Accession: S07453
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   72.3%;   Score 539;   DB 2;   Length 120;
Best Local Similarity   89.3%;   Pred. No. 5.3e-40;
Matches 108;   Conservative   2;   Mismatches 7;   Indels 4;   Gaps 1;

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Qy   20  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
            ||||||||||||||||||||||||||||||||||::||||||||||||||||||||:|||
Db    1  EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy   80  DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
            |||||||||||||||||||||||||||||||::||         |||||||||||||
Db   61  DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR---------GWLRRDAMDYWGQGTSVT 116

Qy  140  V 140
            |
Db  117  V 117
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RESULT 6
S17586
Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S17586
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
forms.
A;Reference number: S17586; MUID:92015240; PMID:1656053
A;Accession: S17586
A;Status: preliminary

Query Match   80.0%;   Score 597;   DB 2;   Length 136;
Best Local Similarity   82.9%;   Pred. No. 5.4e-45;
Matches 116;   Conservative   6;   Mismatches 12;   Indels 6;   Gaps 1;

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Qy    1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
            |||||:::|||||| ||||||||||||||||||||||||||||||:|:||
Db    1  MKCSWVIFFLMAVVIGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDDYMHWVKQRP 60

Qy   61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
            |||||||||||:| ||:|| |:| |||||||| ||:|
Db   61  EQGLEWIGWIDPENGDTQYASKFQGKATMTADTSSNTYLQLSSLTSEDTAVYYCT---- 116

Qy  121  YGNYGVYAMDYWGQGTSVTV 140
            ||   |||||||||||||
Db  117  --TYGAYAMDYWGQGTSVTV 134
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RESULT 3
S52445
Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52445
R;Berdoz, J.; Kraehenbuhl, J.P.
A;Description: Specific amplification by the polymerase chain reaction of rearranged gen
submitted to the EMBL Data Library, November 1994
A;Reference number: S52445
A;Accession: S52445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <BER>
A;Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain: immunoglobulin homology <IMM>

Query Match   76.5%;   Score 570.5;   DB 2;   Length 137;
Best Local Similarity   81.4%;   Pred. No. 1.1e-42;
Matches 114;   Conservative   6;   Mismatches 15;   Indels 5;   Gaps 2;

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Qy    1  MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
            |||||:::||||||| |||||||||||||||| ::|:||
Db    1  MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVRPGALVKPGALVRPGALVRPGA 60

Qy   61  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
            ||||||| ||| || |:| |:| ||| |||||||||||||||||::||||||||
Db   61  EQGLEWIGWIDPENGTVYDPKFQGKASITADTSSNTAYLQLSSLASEDTAVYYCA---Y 117

Qy  121  YGNYGVYAMDYWGQGTSVTV 140
            ||   :|| |||||||:|||
Db  118  YGT--SYWFPYWGQGTLVTV 135
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RESULT 4
PH1403
Ig heavy chain V region (clone micro m- 46-6, 46-12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: PH1403
R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta
J. Exp. Med. 176, 1209-1214, 1992
A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
la virus.
A;Reference number: PH1403; MUID:93018837; PMID:1402663
A;Accession: PH1403
A;Molecule type: DNA
A;Residues: 1-123 <SHI>
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology

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                 GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October 7, 2003, 09:02:30 ; Search time 10.4646 seconds
                                          (without alignments)
                                          629.141 Million cell updates/sec

Title:      US-09-155-739-4
Perfect score: 746
Sequence:   1 MKCSWVMFFLMAVVTGVNSE.........YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:   127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:    127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                               SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	464.5	62.3	139	1	HV07_MOUSE	P01751 mus musculu
2	459	61.5	140	1	HV02_MOUSE	P01746 mus musculu
3	425	57.0	120	1	HV03_MOUSE	P01747 mus musculu
4	422.5	56.6	137	1	HV11_MOUSE	P01755 mus musculu
5	416	55.8	138	1	HV48_MOUSE	P03980 mus musculu
6	411	55.1	117	1	HV09_MOUSE	P01753 mus musculu
7	396	53.1	136	1	HV15_MOUSE	P01749 mus musculu
8	393	52.7	117	1	HV06_MOUSE	P01750 mus musculu
9	393	52.7	117	1	HV49_MOUSE	P06328 mus musculu
10	389	52.1	117	1	HV10_MOUSE	P01754 mus musculu
11	388	52.0	117	1	HV04_MOUSE	P01748 mus musculu
12	381	51.1	117	1	HV52_MOUSE	P06327 mus musculu
13	379	50.8	117	1	HV13_MOUSE	P01757 mus musculu
14	379	50.8	121	1	HV01_MOUSE	P01745 mus musculu
15	378.5	50.7	147	1	HV1C_HUMAN	P01744 homo sapien
16	374	50.1	117	1	HV05_MOUSE	P01749 mus musculu
17	374	50.1	117	1	HV12_MOUSE	P01756 mus musculu
18	372	49.9	117	1	HV14_MOUSE	P01758 mus musculu
19	368.5	49.4	118	1	HV51_MOUSE	P06330 mus musculu
20	367	49.2	117	1	HV1B_HUMAN	P01743 homo sapien
21	360.5	48.3	120	1	HV50_MOUSE	P06329 mus musculu
22	359	48.1	117	1	HV1G_HUMAN	P23083 homo sapien
23	356.5	47.8	136	1	HV16_MOUSE	P01783 mus musculu
24	321.5	43.1	114	1	HV00_MOUSE	P01741 mus musculu
25	316.5	42.4	119	1	HV38_MOUSE	P01808 mus musculu
26	315	42.2	117	1	HV42_MOUSE	P01812 mus musculu
27	314	42.1	117	1	HV1A_HUMAN	P01742 homo sapien
28	312.5	41.9	119	1	HV37_MOUSE	P01807 homo sapien
29	311	41.7	142	1	HV01_RAT	P01805 ratus norv
30	310.5	41.6	119	1	HV40_MOUSE	P01810 mus musculu
31	304	40.8	118	1	HV39_MOUSE	P01809 mus musculu
32	297	39.8	137	1	HV46_MOUSE	P01822 mus musculu
33	297	39.8	144	1	HV26_MOUSE	P01795 mus musculu
34	293.5	39.3	120	1	HV1H_HUMAN	P80421 homo sapien
35	292	39.1	117	1	HV41_MOUSE	P01811 mus musculu
36	291.5	39.1	116	1	HV05_CARAU	P19181 carassius a
37	290	38.9	116	1	HV36_MOUSE	P01806 mus musculu
38	290	38.9	123	1	HV24_MOUSE	P01793 mus musculu
39	288	38.6	117	1	HV3C_HUMAN	P01764 homo sapien
40	285.5	38.3	116	1	HV3T_HUMAN	P01781 homo sapien
41	284.5	38.1	122	1	HV3G_HUMAN	P01768 homo sapien
42	284	38.1	144	1	HV43_MOUSE	P01819 mus musculu
43	284	38.1	146	1	HV2I_HUMAN	P06331 homo sapien
44	282.5	37.9	122	1	HV3A_HUMAN	P01762 homo sapien
45	282	37.8	125	1	HV1F_HUMAN	P06326 homo sapien

```
                               ALIGNMENTS

RESULT 1
HV07_MOUSE
ID   HV07_MOUSE   STANDARD;   PRT;   139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region B1-8/186-2 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   --------------------------------------------------------------------
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC       the European Bioinformatics Institute. There are no restrictions on its
CC       use by non-profit institutions as long as its content is in no way
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CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A90809; MHMS18.
DR   PDB; 1A6U; 27-MAY-98.
DR   PDB; 1A6W; 15-JUL-98.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; 3D-structure.
FT   SIGNAL        1     19
FT   CHAIN        20    139       IG HEAVY CHAIN V REGION B1-8/186-2.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DOMAIN      118    124       D SEGMENT.
FT   DOMAIN      125    139       JH2 SEGMENT.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     139    139
SQ   SEQUENCE   139 AA;   15419 MW;   1B57DD4FD0C9F465 CRC64;
```

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Query Match            62.3%;  Score 464.5;  DB 1;  Length 139;
Best Local Similarity  65.0%;  Pred. No. 1.3e-37;
Matches     91;  Conservative  18;  Mismatches  28;  Indels   3;  Gaps   1;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          :||||||:|| :|| :|||| ||||||||||||||||| :||: :: |||||
Db    1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          :||||||||| :| ||| :: || |||||||| |||||||||||||||:||
Db   61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDY 120

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
          ||: ||||||||||||
Db  121 YGS--SYFDYWGQGTTLTV 137
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RESULT 2
HV02_MOUSE
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ID   HV02_MOUSE     STANDARD;      PRT;   140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 93G7 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   -----------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------
DR   EMBL; J00493; AAA38128.1; -.
DR   PIR; A94264; HVMSG7.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Hybridoma; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    140       IG HEAVY CHAIN V REGION 93G7.
FT   DOMAIN       20    139       IG-LIKE.
FT   NON_TER     140    140
SQ   SEQUENCE   140 AA;  15514 MW;  25A4CBBE31DA5CE8 CRC64;

Query Match            61.5%;  Score 459;  DB 1;  Length 140;
Best Local Similarity  63.6%;  Pred. No. 4.4e-37;
Matches     89;  Conservative  18;  Mismatches  31;  Indels   2;  Gaps   1;

Qy    1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          | |:| ||||||:|| :||||||||||||||:|||| |||:||||||
Db    1 MGWSFIFLFLLSVTAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP 60

Qy   61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          |||||||:|: || : |||| || |||||||||:|:|| |||||||||||:|||||||
Db   61 GQGLEWIGYINPGNGYINYNEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHY 120

Qy  121 YGNYGVYAMDYWGQGTSVTV 140
          |: || :|||||||||:||
Db  121 YG--GSYDFYWGQGTPLTV 138
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RESULT 3
HV03_MOUSE
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ID   HV03_MOUSE     STANDARD;      PRT;   120 AA.
AC   P01747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83131846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
CC   -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC       DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC       CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC       SEGMENT, JH2.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Hybridoma.
FT   DOMAIN        1    111       IG-LIKE.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13307 MW;  FF04E4A167B654AF CRC64;

Query Match            57.0%;  Score 425;  DB 1;  Length 120;
Best Local Similarity  68.3%;  Pred. No. 6.6e-34;
Matches     82;  Conservative  14;  Mismatches  22;  Indels   2;  Gaps   1;

Qy   21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
          |||||||||| :|| |||:|||:|||: |||||| :|||||||||||||||||||:
Db    1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN 60

Qy   81 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
          :||:||||||| |:|  ||||:|||||||:|||||||  | |  :  :|||||||:| |
Db   61 EKFKGKTTLTVDKPSSTAYMQLRSLTSEDSAVYFCARSVYYG--GSYYFDYWGQGTLTV 118
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RESULT 4
HV11_MOUSE
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ID   HV11_MOUSE     STANDARD;      PRT;   137 AA.
AC   P01755;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region S43 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
                    GenCore version 5.1.6
           Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:          October 7, 2003, 09:01:50 ; Search time 46.2545 Seconds
                                             (without alignments)
                                             363.748 Million cell updates/sec

Title:           US-09-155-739-7
Perfect score:   562
Sequence:        1 DIQMTQSPSSLSASVGDRVT.........YCLQYDNLWTFGQGTKVEIK 106

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:          1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_19Jun03:*
                 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
                 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
                 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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                20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
                21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
                22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
                23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
                24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*
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Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB ID			Description
1	562	100.0	106	AAR81321	16		Humanized anti-VLA
2	562	100.0	106	AAW22412	18		Humanised alpha-4
3	562	100.0	126	AAW22419	18		Humanised alpha-4
4	508	90.4	106	AAR81328	16		Mouse anti-VLA-4 a
5	508	90.4	126	AAR81326	16		Mouse VLA-4 antibo
6	508	90.4	126	AAR81332	18		Human VLA-4 reshap
7	508	90.4	126	AAW22409	18		Alpha-4 integrin m
8	488	86.8	359	AAY29913	20		Human MCP-3 and mu
9	488	86.8	361	AAY29911	20		Human IP-10 and mu
10			488	86.8	374	AAY29916 20	Artificial synthet
11			481	85.6	128	AAR60627 15	MEI-14 light chain
12			475.5	84.6	234	AAR13050 12	CD4-specific CDR-g
13			471.5	83.9	107	AAR78970 16	Light chain variab
14			465	82.7	108	AAR93159 17	Murine monoclonal
15			460.5	81.9	128	AAR06252 11	Variable region of
16			460	81.9	637	AAR26983 13	(FRP51)-ETA fusion
17			456	81.1	109	AAW26797 19	Anti-gp54 MAb T16
18			455	81.0	240	AAW85495 16	ScFv(FWP51). Synt
19			455	81.0	241	AAY21882 20	Amino acid sequenc
20			455	81.0	245	AAW26800 19	Anti-gp54 MAb T16
21			453.5	80.7	107	AAR81322 16	Humanized VLA-4 an
22			453.5	80.7	107	AAW22422 18	Humanised alpha-4
23			453	80.6	109	AAR13658 12	Murine OKT4A light
24			452	80.4	241	AAR26981 13	FWP51 fusion prote
25			451.5	80.3	108	AAR65163 16	Human REI monoclon
26			451.5	80.3	129	AAR47207 15	Human/murine IL-1
27			451	80.2	355	AAW35133 18	R. pipiens recombi
28			449.5	80.0	107	AAW86805 19	Variable Light dom
29			449.5	80.0	107	AAW70625 19	Humanised murine a
30			449.5	80.0	107	ABP61194 23	Humanised anti-VEG
31			446.5	79.4	108	AAW10231 18	CDR-grafted light
32			446.5	79.4	110	AAW70673 19	Anti-VEGF humanise
33			446.5	79.4	110	ABP61242 23	Humanised anti-VEG
34			446.5	79.4	234	AAW10233 18	TF8-5G9 CDR-grafte
35			446.5	79.4	237	AAW70703 19	Protein encoded by
36			446.5	79.4	650	ABP61241 23	Phage-display anti
37			445.5	79.3	107	AAW86804 19	Variable Light dom
38			445.5	79.3	107	AAW70623 19	Humanised murine a
39			445.5	79.3	107	ABP61192 23	Humanised anti-VEG
40			444.5	79.1	107	AAW87455 20	Humanised anti-alp
41			444.5	79.1	107	AAB62087 22	Human V1 consensus
42			444.5	79.1	107	AAB60400 22	Consensus human 11
43			444.5	79.1	107	AAB61585 22	Human variable lig
44			444.5	79.1	108	AAW70622 19	Human consensus fr
45			444.5	79.1	108	AAY83345 21	Human consensus se

ALIGNMENTS

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RESULT 1
AAR81321
ID   AAR81321 standard; Protein; 106 AA.
XX
AC   AAR81321;
XX
DT   02-APR-1996  (first entry)
XX
DE   Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Chimeric Mus musculus.
OS   Chimeric Homo sapiens.
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;  95WO-US01219.
XX
PR   25-JAN-1994;  94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
```

```
PT   inflammatory disease.
XX
PS   Claim 9; Page 67; 105pp; English.
XX
CC   The sequence encodes the humanized mouse antibody 21.6 light chain
CC   variable region, La, directed against leukocyte adhesion molecule
CC   VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and
CC   AAQ99892) regions are linked to human constant regions in the
CC   construction of a humanized antibody against VLA-4. The 5' and 3'
CC   ends of the mouse cDNAs are modified using PCR primers (See
CC   AAQ99895-98) and then subcloned into mammalian cell expression vectors
CC   containing human kappa or gamma-1 constant regions. In the humanized
CC   light chain, amino acids L45, L49, L58 and L69 in the human kappa LC
CC   VR framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric
CC   antibodies are transfected into COS cells. The humanized antibodies
CC   can be used for inhibiting adhesion of a leukocyte to an endothelial
CC   cell and for treating inflammatory diseases such as multiple
CC   sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX
SQ   Sequence   106 AA;

Query Match          100.0%;   Score 562;   DB 16;   Length 106;
Best Local Similarity 100.0%;   Pred. No. 1.4e-36;
Matches  106;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||||||||||||||||||||||||||||||||||||||
Db      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106


RESULT 2
AAW22412
ID   AAW22412 standard; Protein; 106 AA.
XX
AC   AAW22412;
XX
DT   08-DEC-1997 (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL La.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1..23
FT                   /label= FR1
FT                   /note= "REI framework region 1"
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          35..49
FT                   /label= FR2
FT                   /note= "REI framework region 2"
FT   Misc-difference 45
FT                   /note= "REI Lys-45 is substd. by Lys of mouse
FT                   21.6 VL, important in supporting the
FT                   CDR2 loop"
FT   Misc-difference 49
FT                   /note= "REI Tyr-49 is substd. by His of mouse
FT                   21.6 VL, located at the binding site"
FT   Region          50..56
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          57..88
FT                   /label= FR3
FT                   /note= "REI framework region 3"
FT   Misc-difference 58
FT                   /note= "REI Val-58 is substd. by Ile of mouse
FT                   21.6 VL, important in supporting the CDR2
FT                   loop"
FT   Misc-difference 69
FT                   /note= "REI Thr-69 is substd. by Arg of mouse
FT                   21.6 VL, involved in antibody-antigen
FT                   binding"
FT   Region          89..96
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          97..106
FT                   /label= FR4
FT                   /note= "REI framework region 4"
FT   Misc-difference 103
FT                   /note= "REI Leu-103 substd. by Val, more typical
FT                   of human kappa light chain J region"
FT   Misc-difference 104
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FT   Misc-difference 106
FT                   /note= "REI Thr-106 substd. by Lys, more typical
FT                   of human kappa light chain J region"
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PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR   WPI; 1997-297879/27.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 25; Fig 6; 107pp; English.
XX
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6. It is
CC   composed of complementarity determining regions (CDRs) from the VL
CC   region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human REI framework. It can be expressed in
CC   mammalian host cells following PCR amplification and mutagenesis
CC   of appropriate fragments of mouse and human DNA sequences. The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibody has a
CC   half-life in the human circulation essentially equivalent to that
CC   of naturally occurring human antibodies.
XX
SQ   Sequence   106 AA;
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              GenCore version 5.1.6
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   October 7, 2003, 09:10:55 ; Search time 13.7051 Seconds
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Title:          US-09-155-739-7
Perfect score:  562
Sequence:       1 DIQMTQSPSSLSASVGDRVT........YCLQYDNLWTFGQGTKVEIK 106

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:       328717

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	562	100.0	106	2	US-08-561-521-7	Sequence 7, Appli
2	562	100.0	106	5	PCT-US95-01219-7	Sequence 7, Appl
3	508	90.4	106	5	US-08-561-521-5	Sequence 5, Appl
4	508	90.4	106	5	PCT-US95-01219-5	Sequence 5, Appl
5	508	90.4	126	2	US-08-561-521-2	Sequence 2, Appl
6	508	90.4	126	2	US-08-561-521-15	Sequence 15, Appl
7	508	90.4	126	5	PCT-US95-01219-2	Sequence 2, Appl
8	508	90.4	126	5	PCT-US95-01219-15	Sequence 15, Appl
9	488	86.8	359	4	US-09-646-028-16	Sequence 16, Appl
10	488	86.8	361	4	US-09-646-028-13	Sequence 13, Appl
11	488	86.8	374	4	US-09-646-028-15	Sequence 15, Appl
12	481	85.6	128	1	US-08-339-582-4	Sequence 4, Appli
13	471.5	83.9	107	5	US-08-888-366-22	Sequence 22, Appl
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15	460	81.9	637	1	US-08-235-838-16	Sequence 16, Appl
16	455	81.0	241	1	US-08-465-473B-11	Sequence 11, Appl
17	455	81.0	241	2	US-08-465-473B-11	Sequence 11, Appl
18	454.5	80.9	108	2	US-08-602-725-29	Sequence 29, Appl
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20	453.5	80.7	107	5	PCT-US95-01219-8	Sequence 8, Appli
21	451	80.2	355	3	US-08-875-811-57	Sequence 57, Appl
22	448.5	79.8	107	2	US-07-934-373C-17	Sequence 17, Appl
23	448.5	79.8	107	3	US-08-437-642B-17	Sequence 17, Appl
24	448.5	79.8	107	3	US-08-146-206C-17	Sequence 17, Appl
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40	443.5	78.9	108	2	US-08-116-247-9	Sequence 9, Appli
41	443.5	78.9	108	4	US-08-557-050-7	Sequence 7, Appli
42	441.5	78.6	107	2	US-08-318-157B-6	Sequence 6, Appli
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ALIGNMENTS

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RESULT 1
US-08-561-521-7
; Sequence 7, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
;    APPLICANT: Bendig, Mary M.
;    APPLICANT: Leger, Olivier J.
;    APPLICANT: Saldanha, Jose
;    APPLICANT: Jones, S. Tarran
;    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION: Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES: 45
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Townsend and Townsend Khourie and Crew
;       STREET: One Market Plaza, Steuart Tower, Suite 2000
;       CITY: San Francisco
;       STATE: California
;       COUNTRY: USA
;       ZIP: 94105
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/561,521
;       FILING DATE:
;       CLASSIFICATION: 424
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US/08/186,269A
;       FILING DATE: 25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Smith, William L.
;       REGISTRATION NUMBER: 30,223
;       REFERENCE/DOCKET NUMBER: 15270-14
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 415-543-9600
;       TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH: 106 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;    MOLECULE TYPE: protein
US-08-561-521-7

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RESULT 2
PCT-US95-01219-7
; Sequence 7, Application PC/TUS9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 106 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US95-01219-7

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Best Local Similarity 100.0%; Pred. No. 1.6e-45;
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; Sequence 5, Application US/08561521
; Patent No. 5840299

GENERAL INFORMATION:
  APPLICANT: Bendig, Mary M.
  APPLICANT: Leger, Olivier J.
  APPLICANT: Saldanha, Jose
  APPLICANT: Jones, S. Tarran
  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
  TITLE OF INVENTION: Adhesion Molecule VLA-4
  NUMBER OF SEQUENCES: 45
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend Khourie and Crew
    STREET: One Market Plaza, Steuart Tower, Suite 2000
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94105
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/561,521
    FILING DATE:
    CLASSIFICATION: 424
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/186,269A
    FILING DATE: 25-JAN-1994
  ATTORNEY/AGENT INFORMATION:
    NAME: Smith, William L.
    REGISTRATION NUMBER: 30,223
    REFERENCE/DOCKET NUMBER: 15270-14
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415-543-9600
    TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 106 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-561-521-5

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Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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; Sequence 5, Application PC/TUS9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA

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                    GenCore version 5.1.6
             Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        October 7, 2003, 09:18:36 ; Search time 26.7677 Seconds
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Title:         US-09-155-739-7
Perfect score: 562
Sequence:      1 DIQMTQSPSSLSASVGDRVT..........YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
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Searched:      587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters:        587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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                                 SUMMARIES
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Match Length	DB	ID	Description	
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2	488	86.8	361	12	US-10-335-394-13	Sequence 13, Appl
3	488	86.8	374	12	US-10-335-394-15	Sequence 15, Appl
4	479.5	85.3	108	9	US-09-229-200A-11	Sequence 11, Appl
5	479.5	85.3	108	9	US-09-229-200A-15	Sequence 15, Appl
6	466.5	83.0	108	9	US-09-229-200A-16	Sequence 16, Appl
7	449.5	80.0	107	9	US-09-056-160B-15	Sequence 15, Appl
8	446.5	79.4	110	9	US-09-056-160B-103	Sequence 103, App
9	446.5	79.4	237	9	US-09-056-160B-100	Sequence 100, App
10	446.5	79.4	491	14	US-10-011-125-2	Sequence 2, Appli
11	445.5	79.3	107	9	US-09-056-160B-13	Sequence 13, Appli
12	444.5	79.1	107	12	US-10-223-880-15	Sequence 5, Appli
13	444.5	79.1	107	15	US-10-268-501-15	Sequence 5, Appli
14	444.5	79.1	108	9	US-09-056-160B-12	Sequence 12, Appl
15	444.5	79.1	109	9	US-09-811-123-6	Sequence 6, Appli
16	444.5	79.1	110	12	US-10-044-896-4	Sequence 4, Appli
17	443.5	78.9	107	10	US-09-999-025-15	Sequence 15, Appl
18	443.5	78.9	107	10	US-09-999-040-15	Sequence 15, Appl
19	443.5	78.9	107	11	US-09-998-817-15	Sequence 15, Appl
20	443.5	78.9	107	11	US-09-999-021-15	Sequence 15, Appl
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23	443.5	78.9	108	15	US-10-267-286A-7	Sequence 7, App
24	443.5	78.9	110	9	US-09-056-160B-105	Sequence 105, App
25	443	78.8	109	9	US-09-229-200A-7	Sequence 7, Appli
26	442.5	78.7	108	9	US-09-056-160B-8	Sequence 8, Appli
27	442.5	78.7	108	14	US-10-153-159-2	Sequence 2, Appli
28	442.5	78.7	108	14	US-10-153-159-16	Sequence 16, Appl
29	442.5	78.7	108	15	US-10-153-176-2	Sequence 2, Appli
30	442.5	78.7	108	15	US-10-153-176-16	Sequence 16, Appl
31	442.5	78.7	131	15	US-10-207-655-256	Sequence 256, App
32	442.5	78.7	266	15	US-10-207-655-260	Sequence 260, App
33	442.5	78.7	550	15	US-10-207-655-270	Sequence 270, App
34	441.5	78.6	107	9	US-09-253-794-6	Sequence 6, Appli
35	439.5	78.2	108	14	US-10-153-159-4	Sequence 4, Appli
36	439.5	78.2	108	15	US-10-153-176-4	Sequence 4, Appli
37	439.5	78.2	110	9	US-09-056-160B-107	Sequence 107, App
38	439.5	78.2	110	9	US-09-056-160B-117	Sequence 117, App
39	439.5	78.2	237	15	US-10-020-786-10	Sequence 10, Appl
40	438.5	78.0	108	9	US-09-905-243-73	Sequence 73, Appl
41	438.5	78.0	109	11	US-09-802-083-4	Sequence 4, Appli
42	438.5	78.0	109	12	US-10-172-785-4	Sequence 4, Appli
43	438.5	78.0	109	15	US-10-165-732A-4	Sequence 4, Appli
44	438.5	78.0	127	10	US-09-809-739-10	Sequence 10, Appl
45	438.5	78.0	214	9	US-09-940-166A-2	Sequence 2, Appl

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RESULT 1
US-10-335-394-16
; Sequence 16, Application US/10335394
; Publication No.US2003013852A1
; GENERAL INFORMATION:
;  APPLICANT:  Kwak, Larry
;  APPLICANT:  Biragyn, Arya
;  TITLE OF INVENTION:  METHODS AND COMPOSITIONS OF
;  TITLE OF INVENTION:  CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
;  FILE REFERENCE: 14014.0316/P
;  CURRENT APPLICATION NUMBER: US/10/335,394
;  CURRENT FILING DATE:  2002-12-31
;  PRIOR APPLICATION NUMBER: US/09/646,028
;  PRIOR FILING DATE: 2000-09-12
;  PRIOR APPLICATION NUMBER: 60/077,745
;  PRIOR FILING DATE: 1998-03-12
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;  LENGTH: 359
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-16

  Query Match             86.8%;  Score 488; DB 12;  Length 359;
  Best Local Similarity   84.9%;  Pred. No. 8.7e-37;
  Matches   90; Conservative    9; Mismatches    7; Indels    0; Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
             ||||||||||||||| |:||||| |||||||:|||| | ||| ||||||||||||||||
Db     233 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 292

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
             ||||||||||:|:|| |||||||||||||||||:| ||||||||||
Db     293 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 338
```

```
Qy    61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
          ||||||||||:|:|:||:|::||||||||||||||  |||:||| 
Db   155 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 200
```

RESULT 4
US-09-229-200A-11
; Sequence 11, Application US/09229200A
; Patent No. US2002009179A1
; GENERAL INFORMATION:
;   APPLICANT: Jolliffe et al.
;   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Johnson & Johnson
;   STREET: One Johnson & Johnson Plaza
;   CITY: New Brunswick
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08933-7003
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;   COMPUTER: IBM
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: <Unknown>
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/229,200A
;   FILING DATE: 13-Jan-1999
;   CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: John W. Wallen, III
;   REGISTRATION NUMBER: 35,403
;   REFERENCE/DOCKET NUMBER: ORT-948
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (858) 784-3239
;   TELEFAX: (908) 524-2808
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 108
;   TYPE: amino acid
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-229-200A-11

Query Match   85.3%; Score 479.5; DB 9; Length 108;
Best Local Similarity   85.8%; Pred. No. 1.5e-36;
Matches 91; Conservative   7; Mismatches   7; Indels   1; Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||| : ||| |: |||||||||||| |||:|||||||:||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCKASPDINNYLNWYQQTPGKAPKLLIYYTSTLQPGVPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
          ||||||||||:|:|:||:|:||||||||||||||| :|||:|||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCQQYDNLIFTFGGGTKLQI 106
```

RESULT 5
US-09-229-200A-15
; Sequence 15, Application US/09229200A
; Patent No. US2002009179A1
; GENERAL INFORMATION:
;   APPLICANT: Jolliffe et al.
;   TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Johnson & Johnson
;     STREET: One Johnson & Johnson Plaza
;     CITY: New Brunswick
;     STATE: NJ
;     COUNTRY: USA
;     ZIP: 08933-7003
;
```

RESULT 2
US-10-335-394-13
; Sequence 13, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
;   APPLICANT: Kwak, Larry
;   APPLICANT: Biragyn, Arya
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
;   TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
;   FILE REFERENCE: 14014.0316/P
;   CURRENT APPLICATION NUMBER: US/10/335,394
;   CURRENT FILING DATE: 2002-12-31
;   PRIOR APPLICATION NUMBER: US/09/646,028
;   PRIOR FILING DATE: 2000-09-12
;   PRIOR APPLICATION NUMBER: 60/077,745
;   PRIOR FILING DATE: 1998-03-12
;   NUMBER OF SEQ ID NOS: 57
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-13

Query Match   86.8%; Score 488; DB 12; Length 361;
Best Local Similarity   84.9%; Pred. No. 8.7e-37;
Matches 90; Conservative   9; Mismatches   7; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||: :||||| ||| |||||||||| |||||||||||||||||
Db   235 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 294

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
          ||||||||||:|::|:|||||||||||||||| ||| ||| :|||
Db   295 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLEIK 340
```

RESULT 3
US-10-335-394-15
; Sequence 15, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
;   APPLICANT: Kwak, Larry
;   APPLICANT: Biragyn, Arya
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
;   TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
;   FILE REFERENCE: 14014.0316/P
;   CURRENT APPLICATION NUMBER: US/10/335,394
;   CURRENT FILING DATE: 2002-12-31
;   PRIOR APPLICATION NUMBER: US/09/646,028
;   PRIOR FILING DATE: 2000-09-12
;   PRIOR APPLICATION NUMBER: 60/077,745
;   PRIOR FILING DATE: 1998-03-12
;   NUMBER OF SEQ ID NOS: 57
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
;   LENGTH: 374
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-15

Query Match             86.8%;  Score 488;  DB 12;  Length 374;
Best Local Similarity   84.9%;  Pred. No. 9.1e-37;
Matches  90;  Conservative   9;  Mismatches   7;  Indels   0;  Gaps   0;

Qy     1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           : |||||||||||||: :|||||| ||| |||||||||| ||| |||||||||||||
Db    95 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 154
```

```
                    GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  7, 2003, 09:09:40 ; Search time 14.9899 Seconds
                                        (without alignments)
                                        680.050 Million cell updates/sec

Title:          US-09-155-739-7
Perfect score:  562
Sequence:       1 DIQMTQSPSSLSASVGDRVT.........YCLQYDNLWTFGQGTKVEIK 106
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:        283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR_76:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Score	Length	DB	ID	Description
1	488	86.8	104	2	S26330		Ig kappa chain v r
2	479	85.2	104	2	S26329		Ig kappa chain v r
3	478	85.1	106	2	C33936		Ig kappa chain v r
4	463.5	82.5	125	2	S09365		Ig kappa chain - m
5	452	80.4	97	2	PH1064		Ig light chain v r
6	446.5	79.4	107	2	PL0270		Ig kappa chain v r
7	443.5	78.9	108	1	K1HURE		Ig kappa chain v-I
8	443.5	78.9	129	2	S52789		Ig kappa chain v-I
9	443	78.8	103	2	S26332		Ig light chain v r
10	440.5	78.4	107	2	PL0272		Ig kappa chain v r
11	440	78.3	94	2	E33730		Ig kappa chain v r
12	439.5	78.2	107	2	PL0269		Ig kappa chain v r
13	439.5	78.2	107	2	PL0271		Ig kappa chain v-I
14	439.5	78.2	108	1	K1HUAU		Ig kappa chain v-I
15	435.5	77.5	108	2	I39154		Ig kappa chain (BR
16	429.5	76.4	110	2	S44118		Ig kappa chain v-J
17	429.5	76.4	127	2	S40367		Ig kappa chain v-J
18	426	75.8	107	2	S36275		Ig lambda chain v
19	424.5	75.5	125	2	S40333		Ig kappa chain v-J
20	421.5	75.0	108	1	K1HULY		Ig kappa chain v-J
21	419.5	74.6	108	1	K1HUAG		Ig kappa chain v-I
22	419.5	74.6	108	1	K1HURY		Ig kappa chain v-I
23	418.5	74.5	123	2	S40331		Ig kappa chain - h
24	415	73.9	109	2	S31998		Ig kappa chain - h
25	414.5	73.8	131	2	S40352		Ig kappa chain v-J
26	414	73.7	124	2	S40336		Ig kappa chain v-J
27	413.5	73.6	108	1	K1HUSW		Ig kappa chain v-I
28	412.5	73.4	108	2	B49047		Ig kappa chain v r
29	412	73.3	106	2	PC2397		anti-tetanus toxin

30	410.5	73.0				S44122	2	Ig kappa chain v r
31	410.5	73.0				S31981	2	Ig kappa chain - h
32	409.5	72.9				K1HUWK	1	Ig kappa chain pre
33	409	72.8				K1HUAR	1	Ig kappa chain v-I
34	408.5	72.7				K1HUWE	1	Ig kappa chain v-I
35	408.5	72.7				S40365	2	Ig kappa chain - h
36	407.5	72.5				A49134	2	Ig kappa chain v-I
37	405.5	72.2				S46371	2	Ig kappa chain v-J
38	405	72.1				S30521	2	Ig kappa chain v r
39	404.5	72.0				S40334	2	Ig kappa chain - h
40	403.5	71.8				PH1063	2	Ig light chain v r
41	403.5	71.8				S36264	2	Ig lambda chain v
42	403.5	71.8				S11240	2	Ig kappa chain v r
43	403	71.7				S43528	2	Ig kappa chain v r
44	403	71.7				S42263	2	Ig kappa chain v r
45	402.5	71.6				K1HUHU	1	Ig kappa chain v-I

```
                            ALIGNMENTS

RESULT 1
S26330
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26330
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26330
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59185; NID:g52316; PIDN:CAA41895.1; PID:g1334063
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match          86.8%;  Score 488; DB 2; Length 104;
Best Local Similarity 85.6%; Pred. No. 1.6e-35;
Matches  89;  Conservative  8;  Mismatches  7;  Indels  0;  Gaps  0;

Qy     1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||||||||:::|||||||| ||| |||||||||| ||||||||||
Db     1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy    61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
           ||||||||||| ||||||||||||||||||||||||||||||:|
Db    61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLE 104

RESULT 2
S26329
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match          85.2%;  Score 479; DB 2; Length 104;
```

```
Best Local Similarity  84.6%;  Pred. No. 9.8e-35;  Indels  0;  Gaps  0;
Matches  88;  Conservative  9;  Mismatches  7;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||:|| ||||||| |||||| ||||||||:||||
Db    1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSLQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
        |||||||||||:||:|:|||||||||||||||||:||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLE 104
```

RESULT 3
C33936
Ig kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831; PMID:2471975
A;Accession: C33936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

```
Query Match  85.1%;  Score 478;  DB 2;  Length 106;
Best Local Similarity  83.0%;  Pred. No. 1.2e-34;
Matches  88;  Conservative  10;  Mismatches  8;  Indels  0;  Gaps  0;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||:|| ||||||| |||||| ||||||||:||||
Db    1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYLAWYQHKPGKGPRLLIHYTSLQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
        |||||||||||:||:|:|||||||||||||||||:||
Db   61 RFSGSGSGRDYSFSISNLDPEEIATYYCLQYDSLYTFGGGTKLEIK 106
```

RESULT 4
S09365
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09365
R;Feddersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene segm
A;Reference number: S09365; MUID:90098844; PMID:2513557
A;Accession: S09365
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

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Query Match  82.5%;  Score 463.5;  DB 2;  Length 125;
Best Local Similarity  83.2%;  Pred. No. 2.6e-33;
Matches  89;  Conservative  7;  Mismatches  7;  Indels  1;  Gaps  1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||:|| ||| ||||||| |||||| ||||||||:||||
Db   18 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSLQPGIPS 77

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW-TFGQGTKVEIK 106
        |||||||||| |:||:||:|||||||||||||||| :|| ||:|||
Db   78 RFSGSGSGSDYSFSISNLGPEDIATYYCLQYDNLLRTFGGGTKLEIK 124
```

RESULT 5
PHI064
Ig light chain V region (clone 202.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PHI064
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PHI064
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

```
Query Match  80.4%;  Score 452;  DB 2;  Length 97;
Best Local Similarity  85.6%;  Pred. No. 2e-32;
Matches  83;  Conservative  8;  Mismatches  6;  Indels  0;  Gaps  0;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        |||||||||||||||:|| ||||||| |||||| ||||||||:||||
Db    1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSLQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTF 97
        |||||||||||:||:|:|||||||||||||||||:||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTF 97
```

RESULT 6
PL0270
Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0270
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

```
Query Match  79.4%;  Score 446.5;  DB 2;  Length 107;
Best Local Similarity  79.4%;  Pred. No. 6.5e-32;
Matches  85;  Conservative  11;  Mismatches  10;  Indels  1;  Gaps  1;

Qy    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
        ||||||||||||||||:|| |||||| |||||| |||||| |:||||
Db    1 DIQMTQSPCSLSASLGDKVTITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
        |||||||||| |:||:||:|||||||||||||||| |:|| ||:|||
Db   61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107
```

RESULT 7
K1HURE

```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  7, 2003, 09:02:30 ; Search time 7.92323 Seconds
                                         (without alignments)
                                         629.141 Million cell updates/sec

Title:          US-09-155-739-7
Perfect score:  562
Sequence:       1 DIQMTQSPSSLSASVGDRVT.........YCLQYDNLWTFGQGTKVEIK 106

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:    127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SwissProt_41:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	443.5	78.9	108	1	KV1O_HUMAN	P01607 homo sapien
2	439.5	78.2	108	1	KV1B_HUMAN	P01594 homo sapien
3	421.5	75.0	108	1	KV1M_HUMAN	P01605 homo sapien
4	419.5	74.6	108	1	KV1A_HUMAN	P01593 homo sapien
5	419.5	74.6	108	1	KV1P_HUMAN	P01608 homo sapien
6	419.5	74.6	108	1	KV1Y_HUMAN	P80362 homo sapien
7	413.5	73.6	108	1	KV1Q_HUMAN	P01609 homo sapien
8	409.5	72.9	129	1	KV1W_HUMAN	P04431 homo sapien
9	409	72.8	107	1	KV1D_HUMAN	P01596 homo sapien
10	408	72.7	108	1	KV1R_HUMAN	P01610 homo sapien
11	402.5	71.6	108	1	KV1H_HUMAN	P01600 homo sapien
12	397.5	70.7	108	1	KV1F_HUMAN	P01598 homo sapien
13	396.5	70.6	108	1	KV1V_HUMAN	P04430 homo sapien
14	390.5	69.5	108	1	KV1K_HUMAN	P01603 homo sapien
15	388.5	69.1	108	1	KV1E_HUMAN	P01597 homo sapien
16	386.5	68.8	108	1	KV1L_HUMAN	P01604 homo sapien
17	385.5	68.6	108	1	KV1N_HUMAN	P01606 homo sapien
18	384.5	68.4	108	1	KV1C_HUMAN	P01595 homo sapien
19	383.5	68.2	108	1	KV1G_HUMAN	P01599 homo sapien
20	383.5	68.2	129	1	KV1X_HUMAN	P04432 homo sapien
21	381.5	67.9	108	1	KV1S_HUMAN	P01611 homo sapien
22	376.5	67.0	134	1	KV4C_HUMAN	P06314 homo sapien
23	371.5	66.1	108	1	KV5J_MOUSE	P01643 mus musculu
24	368	65.5	117	1	KV1J_HUMAN	P01602 homo sapien
25	366.5	65.2	128	1	KV5E_MOUSE	P01637 mus musculu
26	365	64.9	133	1	KV4B_HUMAN	P06313 homo sapien
27	364.5	64.9	108	1	KV5O_MOUSE	P01648 mus musculu
28	363.5	64.7	108	1	KV5N_MOUSE	P01647 mus musculu
29	362	64.4	109	1	KV1T_HUMAN	P01612 homo sapien
30	362	64.4	117	1	KV1I_HUMAN	P01601 homo sapien
31	361.5	64.3	108	1	KV5K_MOUSE	P01644 mus musculu
32	359.5	64.0	108	1	KV5M_MOUSE	P01646 mus musculu
33	358.5	63.8	108	1	KV5L_MOUSE	P01645 mus musculu
34	356.5	63.4	112	1	KV1U_HUMAN	P01613 homo sapien
35	348.5	62.0	114	1	KV4A_HUMAN	P01625 homo sapien
36	348	61.9	129	1	KV3H_HUMAN	P04207 homo sapien
37	346	61.6	129	1	KV3M_HUMAN	P18136 homo sapien
38	345.5	61.5	108	1	KV5T_MOUSE	P01653 mus musculu
39	345	61.4	115	1	KV5F_MOUSE	P01638 mus musculu
40	341.5	60.8	108	1	KV5Q_MOUSE	P01650 mus musculu
41	341	60.7	109	1	KV3E_HUMAN	P01623 homo sapien
42	340.5	60.6	108	1	KV5S_MOUSE	P01652 mus musculu
43	339.5	60.4	108	1	KV5U_MOUSE	P04946 mus musculu
44	339	60.3	109	1	KV3D_HUMAN	P01622 homo sapien
45	339	60.3	109	1	KV3F_HUMAN	P01624 homo sapien

ALIGNMENTS

```
RESULT 1
KV1O_HUMAN
ID   KV1O_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A91663; KIHURE.
DR   PDB; 1REI; 17-FEB-84.
DR   PDB; 1AR2; 12-NOV-97.
DR   PDB; 1BWW; 29-DEC-99.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88
FT   STRAND        4      7
```

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FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       44     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   STRAND       60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       85     90
FT   STRAND       97     98
FT   STRAND      102    106
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;

Query Match             78.9%;
Best Local Similarity   81.1%;   Pred. No. 4.9e-40;
Matches    86;  Conservative    9;  Mismatches   10;  Indels     1;  Gaps     1;

Qy     1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||||||||||||  |: ||:|:  |:| |:||:|: |:||| |:||
Db     1  DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy    61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
          ||||||||  :||||||||||||||||||  |: :||||||||:|
Db    61  RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106


RESULT 2
KV1B_HUMAN
ID   KV1B_HUMAN     STANDARD;       PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the
RT   Bence-Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC       MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC       REGION OF THE KAPPA CHAIN REI.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A91653; KIHUAU.
DR   PDB; 1JV5; 30-JAN-02.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;

Query Match             78.2%;
Best Local Similarity   79.4%;   Score 439.5;  DB 1;  Length 108;
Matches    85;  Conservative    8;  Mismatches   13;  Indels     1;  Gaps     1;

Qy     1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||||||||||||  |: ||:|: |:| |:||:|: |:||| |:||
Db     1  DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy    61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          ||||||||  :||||||||||||||||||  |||  |||||||||||
Db    61  RFSGSGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107


RESULT 3
KV1M_HUMAN
ID   KV1M_HUMAN     STANDARD;       PRT;   108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Lay.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human
RT   IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT   specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
CC   -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC       CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC       WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01871; KIHULY.
DR   HSSP; P01607; 1REI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
```

OM protein - protein search, using sw model

Copyright   GenCore version 5.1.6
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Run on: October 7, 2003, 09:09:15 ; Search time 37.903 Seconds
                                          (without alignments)
                                          721.673 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.........YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   SPTREMBL_23:*
     1: sp_archea:*
     2: sp_bacteria:*
     3: sp_fungi:*
     4: sp_human:*
     5: sp_invertebrate:*
     6: sp_mammal:*
     7: sp_mhc:*
     8: sp_organelle:*
     9: sp_phage:*
    10: sp_plant:*
    11: sp_rodent:*
    12: sp_virus:*
    13: sp_vertebrate:*
    14: sp_unclassified:*
    15: sp_rvirus:*
    16: sp_bacteriap:*
    17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	428.5	76.2	108	4	Q9UL77	Q9ul77 homo sapien
2	418	74.4	241	11	Q921A6	Q921a6 mus musculu
3	414	73.7	107	4	Q96SA9	Q96sa9 homo sapien
4	406.5	72.3	108	4	Q9UL70	Q9ul70 homo sapien
5	395	70.3	107	4	Q9UL81	Q9ul81 homo sapien
6	385.5	68.6	108	4	Q9UL79	Q9ul79 homo sapien
7	384.5	68.4	234	11	Q9R1A5	Q9r1a5 mus musculu
8	379.5	67.5	233	11	Q91WS9	Q91ws9 mus musculu
9	369.5	65.7	234	11	Q8R062	Q8r062 mus musculu
10	365.5	65.0	116	4	Q96PF6	Q96pf6 homo sapien
11	362.5	64.5	107	11	Q9JL84	Q9jl84 mus musculu
12	355.5	63.3	234	11	Q91WF8	Q91wf8 mus musculu
13	353.5	62.9	109	11	Q920E6	Q920e6 mus musculu
14	342.5	60.9	234	4	Q8NEK1	Q8nek1 homo sapien
15	337.5	60.1	298	11	Q9QYF0	Q9qyf0 mus musculu
16	336.5	59.9	108	4	Q9UL83	Q9ul83 homo sapien
17	335.5	59.7	234	11	Q8VCP0	Q8vcp0 mus musculu
18	332	59.1	109	4	Q9UL85	Q9ul85 homo sapien
19	331	58.9	109	4	Q9UL78	Q9ul78 homo sapien
20	329	58.5	109	4	Q9UL86	Q9ul86 homo sapien
21	322.5	57.4	127	11	Q925S9	Q925s9 mus musculu
22	321.5	57.2	108	11	Q8VIJ0	Q8vij0 mus musculu
23	314	55.9	112	11	Q8K1F3	Q8k1f3 mus musculu
24	313.5	55.8	234	11	Q8R028	Q8r028 mus musculu
25	310	55.2	134	11	Q8VDD0	Q8vdd0 mus musculu
26	307.5	54.7	107	11	Q9ER29	Q9er29 mus musculu
27	307	54.6	114	11	Q8K1F1	Q8k1f1 mus musculu
28	306.5	54.5	111	11	Q920E9	Q920e9 mus musculu
29	302.5	53.8	99	11	Q9JL74	Q9jl74 mus musculu
30	302	53.7	112	11	Q8K1F2	Q8k1f2 mus musculu
31	297	52.8	106	5	Q9U410	Q9u410 schistosoma
32	294	52.3	238	11	Q99M37	Q99m37 mus musculu
33	292.5	52.0	114	4	Q9UL80	Q9ul80 homo sapien
34	289	51.4	112	11	Q8K1F0	Q8k1f0 mus musculu
35	284.5	50.6	101	11	Q9JL78	Q9jl78 mus musculu
36	284	50.5	235	11	Q91W12	Q91w12 mus musculu
37	281.5	50.1	97	11	Q9JL76	Q9jl76 mus musculu
38	279	49.6	239	4	Q8NEK0	Q8nek0 homo sapien
39	279	49.6	239	4	Q8TCD0	Q8tcd0 homo sapien
40	278	49.5	239	11	Q8VC55	Q8vc55 mus musculu
41	278	49.5	239	11	Q8K0F8	Q8k0f8 mus musculu
42	277	49.3	238	11	Q8VCI6	Q8vci6 mus musculu
43	273.5	48.7	109	6	Q9N0W5	Q9n0w5 oryctolagus
44	269.5	48.0	103	11	Q9JL80	Q9jl80 mus musculu
45	255	45.4	104	11	Q9JL82	Q9jl82 mus musculu

ALIGNMENTS

RESULT 1
Q9UL77
ID   Q9UL77   PRELIMINARY;   PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035037; AAD56273.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA;   11738 MW;   C06681716C4D16F3 CRC64;

Query Match   76.2%;   Score 428.5; DB 4;   Length 108;
Best Local Similarity   76.6%;   Pred. No. 5.1e-41;
Matches   82; Conservative   8; Mismatches   16; Indels   1; Gaps   1;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||||||||||||| |: |: |: ||||| |||| |||| |||| |:|| |:||

Left column:

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Db     1  DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy    61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
             ||||||||  |:| ||||||||||  ||||  ||:||| || |||||
Db    61  RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGESTKVEIK 107

RESULT 2
Q921A6
ID    Q921A6;                    PRELIMINARY;    PRT;    241 AA.
AC    Q921A6;
DT    01-DEC-2001 (TrEMBLrel. 19, Created)
DT    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE    Anti-CEA 79 single chain Fv fragment (Fragment).
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=98170165; PubMed=9509426;
RA    Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA    Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT    "Cloning and characterization of cDNAs encoding VH and VL of a
RT    monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT    generation of a single-chain Fv molecule (scFv).";
RL    Mol. Cells 7:816-819(1997).
DR    EMBL; U88067; AAB48044.1; -.
DR    InterPro; IPR007110; Ig-like.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003596; Ig_v.
DR    Pfam; PF00047; ig; 2.
DR    SMART; SM00406; IGv; 2.
DR    PROSITE; PS50835; IG_LIKE; 2.
FT    NON_TER    1    1
FT    NON_TER  241  241
SQ    SEQUENCE  241 AA;  26086 MW;  0276887248E9C771 CRC64;

Query Match          74.4%;  Score 418;  DB 11;  Length 241;
Best Local Similarity   73.6%;  Pred. No. 2.2e-39;
Matches   78;  Conservative  12;  Mismatches  16;  Indels   0;  Gaps   0;

Qy     1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
             ||::|||||||||  :||||||||| :|||||||| || ||| || ||   ||||||||||
Db   134  DIELTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRSAHTLHIYIQPGIPS 193

Qy    61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
             ||||||||||:|:|||||||||||||||||||||  |||:||||:||:|
Db   194  RFSGSGSGRDYSFSISNLEPEDIATYYCLHYDNLHFGGGTKLELK 239

RESULT 3
Q96SA9
ID    Q96SA9;                    PRELIMINARY;    PRT;    107 AA.
AC    Q96SA9;
DT    01-DEC-2001 (TrEMBLrel. 19, Created)
DT    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE    Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE    variable region (Fragment).
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=98375893; PubMed=9712075;
RA    Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT    "Molecular analysis of polyreactive monoclonal antibodies from
RT    rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT    antibody v region genes.";
RL    J. Immunol. 161:2020-2031(1998).
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Right column:

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DR     EMBL; U96396; AAB68785.1; -.
DR     InterPro; IPR007110; Ig-like.
DR     InterPro; IPR003006; Ig_MHC.
DR     InterPro; IPR003596; Ig_v.
DR     Pfam; PF00047; ig; 1.
DR     SMART; SM00406; IGv; 1.
DR     PROSITE; PS50835; IG_LIKE; 1.
FT     NON_TER    1    1
FT     NON_TER  107  107
SQ     SEQUENCE  107 AA;  11520 MW;  4BB43E9C5B577F16 CRC64;

Query Match          73.7%;  Score 414;  DB 4;  Length 107;
Best Local Similarity   75.5%;  Pred. No. 2.2e-39;
Matches   80;  Conservative   9;  Mismatches  17;  Indels   0;  Gaps   0;

Qy    1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
            |||||||||||||| :|||| :|: |||| || || ||:|||:|||:||||||||||
Db    1  DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

Qy   61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
            ||||||||| |:| ||||||||||||:| |||||:|| ||||||||
Db   61  RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLTFGGGTKVEIK 106

RESULT 4
Q9UL70
ID    Q9UL70;                    PRELIMINARY;    PRT;    108 AA.
AC    Q9UL70;
DT    01-MAY-2000 (TrEMBLrel. 13, Created)
DT    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE    Myosin-reactive immunoglobulin light chain variable region
DE    (Fragment).
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=98277139; PubMed=9614934;
RA    Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA    Young D.C.;
RT    "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT    fetus.";
RL    Clin. Immunol. Immunopathol. 87:184-192(1998).
DR    EMBL; AF035044; AAD56280.1; -.
DR    HSSP; P01607; 1REI.
DR    InterPro; IPR007110; Ig-like.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003596; Ig_v.
DR    Pfam; PF00047; ig; 1.
DR    SMART; SM00406; IGv; 1.
DR    PROSITE; PS50835; IG_LIKE; 1.
FT    NON_TER    1    1
FT    NON_TER  108  108
SQ    SEQUENCE  108 AA;  11633 MW;  B7BEDC3E41FCCA37 CRC64;

Query Match          72.3%;  Score 406.5;  DB 4;  Length 108;
Best Local Similarity   72.9%;  Pred. No. 1.6e-38;
Matches   78;  Conservative  12;  Mismatches  16;  Indels   1;  Gaps   1;

Qy    1  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
            |||||||||||||| :|||| :||: || |||| || || ||:|||:|||:||||||||||
Db    1  DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60

Qy   61  RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGGGTKVEIK 106
            ||||||||| |:| ||||||||||||::  ::: ||| |||||
Db   61  RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107

RESULT 5
Q9UL81
ID    Q9UL81                     PRELIMINARY;    PRT;    107 AA.
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